

CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: 60/336,695  
PRIOR FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: 10/226,294  
PRIOR FILING DATE: 2002-08-23  
PRIOR APPLICATION NUMBER: 60/314,381  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 09/899,059  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: 60/278,449  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: 60/216,879  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 09/559,230  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: 60/180,908  
PRIOR FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 60/134,067  
PRIOR FILING DATE: 1999-05-13  
PRIOR APPLICATION NUMBER: 60/132,227  
PRIOR FILING DATE: 1999-05-03  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 44  
LENGTH: 177  
TYPE: PRT  
ORGANISM: human  
US-10-310-793-44

Query Match 100.0%; Score 951; DB 14; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAORSSWKLMLFCSIWMLFLCSPSWLIFIFLOLETAKEPCMA 60  
DB 1 MCLSHLENMPLSHSRTOGAORSSWKLMLFCSIWMLFLCSPSWLIFIFLOLETAKEPCMA 60  
QY 61 KFGPLPSKQWASSEPCVNVKSDWKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKN 120  
DB 61 KFGPLPSKQWASSEPCVNVKSDWKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKN 120  
QY 121 KDMIQTLTKSKIONVGGTYELHVGDTIDLIENSEHOVLKNNYWGIIILANPOFIS 177  
DB 121 KDMIQTLTKSKIONVGGTYELHVGDTIDLIENSEHOVLKNNYWGIIILANPOFIS 177

RESULT 6  
US-10-202-062-40  
Sequence 40, Application US/10202062  
Publication No. US20040038349A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.,  
TITLE OF INVENTION: Heteromultimeric TNF ligand Family members  
FILE REFERENCE: PFS59  
CURRENT APPLICATION NUMBER: US/10/202,062  
CURRENT FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/307,838  
PRIOR FILING DATE: 2001-07-27  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 40  
LENGTH: 177  
TYPE: PRT  
ORGANISM: human  
US-10-202-062-40

Query Match 100.0%; Score 951; DB 15; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MCLSHLENMPLSHSRTOGAORSSWKLMLFCSIWMLFLCSPSWLIFIFLOLETAKEPCMA 60  
DB 1 MCLSHLENMPLSHSRTOGAORSSWKLMLFCSIWMLFLCSPSWLIFIFLOLETAKEPCMA 60

DB 1 MCLSHLENMPLSHSRTOGAORSSWKLMLFCSIWMLFLCSPSWLIFIFLOLETAKEPCMA 60  
QY 61 KFGPLPSKQWASSEPCVNVKSDWKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKN 120  
DB 61 KFGPLPSKQWASSEPCVNVKSDWKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKN 120  
QY 121 KDMIQTLTKSKIONVGGTYELHVGDTIDLIENSEHOVLKNNYWGIIILANPOFIS 177  
DB 121 KDMIQTLTKSKIONVGGTYELHVGDTIDLIENSEHOVLKNNYWGIIILANPOFIS 177

RESULT 7  
US-09-345-790-2  
Sequence 2, Application US/09345790  
Patent No. US2002009198A1  
GENERAL INFORMATION:  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ni, Jian  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: Human Endokine Alpha  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 08/912,227  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/912,227  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488, 0470001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
FAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 169 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-345-790-2

Query Match 95.3%; Score 906; DB 9; Length 169;  
Best Local Similarity 100.0%; Pred. No. 1.1e-87;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MPLSHSRTOGAORSSWKLMLFCSIWMLFLCSPSWLIFIFLOLETAKEPCMAKFGPLPSK 68  
DB 1 MPLSHSRTOGAORSSWKLMLFCSIWMLFLCSPSWLIFIFLOLETAKEPCMAKFGPLPSK 60  
QY 69 WQVASSSEPCVNVKSDWKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKNQDMQTLT 128  
DB 61 WQVASSSEPCVNVKSDWKLEILLONGYLYIGQVAPNANNVDAPEFVRLYKNQDMQTLT 120  
QY 129 NKSKIONVGGTYELHVGDTIDLIENSEHOVLKNNYWGIIILANPOFIS 177  
DB 121 NKSKIONVGGTYELHVGDTIDLIENSEHOVLKNNYWGIIILANPOFIS 169  
RESULT 8



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 2, 2004, 12:26:56 ; Search time 40 Seconds  
(without alignments)  
425.759 Million cell updates/sec

Title: US-10-080-455-1

Perfect score: 951  
Sequence: 1 MCISHLEMPJSHSRTOGAO.....VLKNNTYWGILLANPQFIS 177

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	82	8.6	1188	2	A71621	protein with 5'-3'
2	79.5	8.4	665	2	T18979	hypothetical prote
3	79.5	8.4	851	2	T51545	receptor protein k
4	78	8.2	564	2	S73405	hexosophosphate tr
5	77.5	8.1	352	2	D82442	probable peptide A
6	77.5	8.1	880	2	S49627	regulatory protein
7	77	8.1	326	1	VGXRDS	glycoprotein vp7 p
8	77	8.1	326	1	VGXRHN	glycoprotein vp7 p
9	77	8.1	326	1	VGXRHU	glycoprotein vp7 p
10	76.5	8.0	209	2	A86736	tumor necrosis fac
11	76	8.0	525	2	E70125	hypothetical prote
12	75.5	7.9	222	2	S51934	hypothetical prote
13	75.5	7.9	314	2	I50811	MMS-box protein d
14	75.5	7.9	686	2	T20898	hypothetical prote
15	75.5	7.9	686	2	C89921	hypothetical prote
16	75.5	7.9	3890	2	B35216	hypothetical prote
17	75	7.9	129	2	T28230	FP14 protein - low
18	75	7.9	575	2	S23052	ORF MSY069 probabl
19	74.5	7.8	233	1	A48976	tumor necrosis fac
20	74.5	7.8	465	2	T41511	GFP-binding regula
21	74.5	7.8	471	2	S28476	probable dolicho
22	74.5	7.8	543	2	S68467	ribL protein WC024
23	74.5	7.8	974	2	D89057	CD40 receptor-assc
24	74.5	7.8	356	2	JC7660	protein KO9H1.1 f
25	74	7.8	567	2	T49272	G protein alpha sub
26	74	7.8	568	2	A55960	CD40 receptor-assc
27	74	7.8	757	2	P96518	CD40 receptor-assc
28	73.5	7.7	345	2	E71858	protein T2E6.10 (l
29	73.5	7.7	345	2	E71858	hypothetical prote

30	73.5	7.7	504	2	T47446	hypothetical prote
31	73.5	7.7	609	1	A43458	replication protei
32	73.5	7.7	650	2	J07937	transcription acti
33	73	7.7	166	2	S12723	interferon gamma p
34	73	7.7	326	1	VGXRS	glycoprotein VP7 p
35	73	7.7	326	1	VGXRS3	glycoprotein VP7 p
36	73	7.7	1274	2	I40813	neurotoxin type F
37	72.5	7.6	277	2	T46209	hypothetical prote
38	72.5	7.6	442	2	T18917	hypothetical prote
39	72.5	7.6	1510	2	C84727	probable glucan sy
40	72	7.6	393	2	D75207	hypothetical prote
41	72	7.6	447	2	AD2474	hypothetical prote
42	72	7.6	477	2	S32223	penicillin-binding
43	72	7.6	486	2	F35965	probable purine nu
44	72	7.6	545	2	S46151	hypothetical prote
45	72	7.6	1447	2	T15200	hypothetical prote

## ALIGNMENTS

## RESULT 1

A71621  
protein with 5'-3', exonuclease domain (Kem-1 family) PFB0205C - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 09-Jul-2004  
C:Accession: A71621  
R:Gardner, M.J.; Tettehlin, H.; Carnucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.  
Science 282, 1126-1132, 1998  
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A:Reference number: A71600; MID:19021743; PMID:9804551  
A:Accession: A71621  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1188 <GAR>  
A:Cross-references: UNIPROT:O96143; GB:AE001380; GB:AE001362; NID:G3845120; PTDN:AACT18  
A:Experimental source: clone 3D7  
C:Genetics:  
A:Gene: PFB0205C

	Query Match	8.6%;	Score 82;	DB 2;	Length 1188;	
	Best Local Similarity	30.4%;	Pred. No. 19;			
	Matches	38;	Conservative	11;	Mismatches	36; Indels 40; Gaps 9
Qy	41 FSWLFIPIOLETAKPCMAKFG-PLPSKMOMASSEPPCV---- <td>:</td> <td>:</td> <td>:</td> <td>:</td> <td>:</td>	:	:	:	:	:
Dd	7 YMWLVLEFFFLD-----LAKGIGLGHKM-VINNPFSCXIVDRNLTIDMNCGIKLEKA 59	:	:	:	:	:
Qy	91 Q-----NGLYILYGGVAANMANNYAVAPPEVLYLNKKRMDITLFNKSKION 135	:	:	:	:	:
Dd	60 KKGHKHNHGDDNNGDNDNNYDNNVDNNDOCEIN-RNIKKD--NTYDN-----N 111	:	:	:	:	:
Qy	136 VGGTY 140	:	:	:	:	:
Dd	112 INNTY 116	:	:	:	:	:

## RESULT 2

T18979  
hypochelical protein C06B3.2 - *Caenorhabditis elegans*  
C|Species: *Caenorhabditis elegans*  
C|Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C|Accession: T18979  
R|Percy, C.  
submitted to the EMBL Data Library, July 1996  
A|Reference number: Z19056  
A|Accession: T18979  
A|Status: preliminary; translated from GB/EMBL/DBJ  
A|Molecule type: DNA  
A|Residues: 1-665 <MI>  
A|Cross-References: UNIPROT:O17701; EMBL:Z77652; PIDN:CA801113.1; GSPDB:GN00023; CESP:  
A|Experimental source: clone C06B3





S49627  
regulatory protein ARG2 - yeast (Saccharomyces cerevisiae)  
N/Alternate names: protein YML099c  
C/Species: Saccharomyces cerevisiae  
C/Date: 02-Dec-1994 #sequence\_revision 10-Feb-1995 #text\_change 16-Aug-2004  
C/Accession: S49627; A25064  
R/Genies: S.; Bowman, S.  
submitted to the EMBL Data Library, November 1994  
A/Accession: S49627  
A/Molecule type: DNA  
A/Residues: 1-880 <GEN>  
A/Cross-references: UNIPROT:P05085; EMBL:Z46660; NID:9575702; PIDD:CAA86638.1; PID:95757  
R/Messenguy, F.; Dubois, E.; Descamps, F.  
Eur. J. Biochem. 157, 77-81, 1986  
A/Title: Nucleotide sequence of the ARG2 regulatory gene and amino acid sequence homol  
A/Reference number: A25064; MUID:86220196; PMID:3709534  
A/Accession: A25064  
A/Molecule type: DNA  
A/Residues: 1-3,'F',5-128,'L',132-282,'V',284-344,'V',346-365,'Q',367-548,'A',55  
C/Genetics:  
A/Gene: SGD:ARG81; ARG2  
A/Cross-references: MIPS:YML099c; SGD:S0004565  
A/Map position: 13L  
C/Superfamily: GAL4 zinc binuclear cluster homology  
C/Keywords: DNA binding; nucleus  
F/16-53/Domain: GAL4 zinc binuclear cluster homology <GAL4>  
  
Query Match 8.1%; Score 77.5; DB 2; Length 880;  
Best Local Similarity 22.8%; Pred. No. 35;  
Matches 37; Conservative 35; Mismatches 54; Indels 37; Gaps 8;  
  
QY 45 IFIFLOI--ETAKPCMAK-----FGPLPSKQMASEPPCVNKV----- 82  
Db 555 IFEFKLIOQSTALDKRAEIVILBSEBDNKPLDTNATTSSEPPVADVQEGIFRE 614  
QY 83 ---SPWK--LEILLQNGLYLIYQVAPNA---YNDVAFPEVRLYKMKMIGTLTKSK 132  
Db 615 ALNENDKIHIEFVEKITVNSADSPFSSTPPIFTNIA---TESYNNKSDISKVSKTD 671  
QY 133 IQNVGGTYELH-VGDTIDLIENSEHOVLKNTYWGIIILANPQ 174  
Db 672 -ENITGDSLYGLPNSLILFSDCVRIVRNEYNNLYLTPVPR 713  
  
RESULT 7  
VGKRS  
glycoprotein VP7 precursor - human rotavirus A (serotype 2 strain DS1)  
N/Alternate names: outer capsid protein VP7  
C/Species: human rotavirus A  
C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C/Accession: E27620  
R/Green, K.Y.; Midhun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.; F  
Virology 161, 153-159, 1987  
A/Title: Comparison of the amino acid sequences of the major neutralization protein of  
A/Reference number: A27620; MUID:88044489; PMID:2823458  
A/Accession: E27620  
A/Molecule type: genomic RNA  
A/Residues: 1-326 <GRE>  
A/Cross-references: UNIPROT:P11850  
C/Genetics:  
A/Map position: segment 9  
C/Superfamily: rotavirus glycoprotein VP7  
C/Keywords: coat protein; glycoprotein; transmembrane protein  
F/1-23/Domain: signal sequence #status predicted <SIG>  
F/24-36/Product: glycoprotein VP7 #status predicted <GPV>  
F/32-48/Region: hydrophobic #status predicted  
F/59,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
Query Match 8.1%; Score 77; DB 1; Length 326;  
Best Local Similarity 22.8%; Pred. No. 12;  
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY 26 LMLFCSTVMLPLFC-----SFSWLIFIFLOLEFAKEPCMAK-----FGPLPSKQW 71  
Db 10 LTLISITILLNLYIKTITNTMDIIFRFLILALISFPVATQYGMVLPITGSLDAVYTN 69  
QY 72 ASSEPP-----CV-----NKVSPWKLEILLQNGLYLIYQVAPNA---NYNDVAFEV 115  
Db 70 STSGEPFLSTLCLYPAEAKNEISDDEMENTISQFLTRGWPISGVYFKDYNDINTFSV 129  
QY 116 --RLYNNKMDIQTITNSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILANP 173  
Db 130 NPQLYCDYNNV-----LMRYDNTSELDASELADLIINE-----W-----LCNP 167  
QY 174 QFTS 177  
Db 168 MDIS 171  
  
RESULT 8  
VGKRN  
glycoprotein VP7 precursor - human rotavirus A (serotype 2 strain HN126)  
N/Alternate names: outer capsid protein VP7  
C/Species: human rotavirus A  
C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C/Accession: F27620  
R/Green, K.Y.; Midhun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.; F  
Virology 161, 153-159, 1987  
A/Title: Comparison of the amino acid sequences of the major neutralization protein of  
A/Reference number: A27620; MUID:88044489; PMID:2823458  
A/Accession: F27620  
A/Molecule type: genomic RNA  
A/Residues: 1-326 <GRE>  
A/Cross-references: UNIPROT:P11851  
C/Genetics:  
A/Map position: segment 9  
C/Superfamily: rotavirus glycoprotein VP7  
C/Keywords: coat protein; glycoprotein; transmembrane protein  
F/1-23/Domain: signal sequence #status predicted <SIG>  
F/24-36/Product: glycoprotein VP7 #status predicted <GPV>  
F/32-48/Region: hydrophobic #status predicted  
F/59,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
Query Match 8.1%; Score 77; DB 1; Length 326;  
Best Local Similarity 22.8%; Pred. No. 12;  
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;  
  
QY 26 LMLFCSTVMLPLFC-----SFSWLIFIFLOLEFAKEPCMAK-----FGPLPSKQW 71  
Db 10 LTLISITILLNLYIKTITNTMDIIFRFLILALISFPVATQYGMVLPITGSLDAVYTN 69  
QY 72 ASSEPP-----CV-----NKVSPWKLEILLQNGLYLIYQVAPNA---NYNDVAFEV 115  
Db 70 STSGEPFLSTLCLYPAEAKNEISDDEMENTISQFLTRGWPISGVYFKDYNDINTFSV 129  
QY 116 --RLYNNKMDIQTITNSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILANP 173  
Db 130 NPQLYCDYNNV-----LMRYDNTSELDASELADLIINE-----W-----LCNP 167  
QY 174 QFTS 177  
Db 168 MDIS 171  
  
RESULT 9  
VGKRN  
glycoprotein VP7 precursor - human rotavirus A  
N/Alternate names: outer capsid protein VP7  
C/Species: human rotavirus A  
C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C/Accession: G27620; A93520; A04134  
R/Green, K.Y.; Midhun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.; F  
Virology 161, 153-159, 1987  
A/Title: Comparison of the amino acid sequences of the major neutralization protein of  
A/Reference number: A27620; MUID:88044489; PMID:2823458

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A:Accession: G276620
A:Molecule type: genomic RNA
A:Residues: 1-326 <GRB>
A:Cross-references: UNIPROT:P04328
A:Experimental source: serotype 2 strain HUS
R:Dyall-Smith, M.L.; Holmes, I.H.
Nucleic Acids Res. 12, 3973-3982, 1984
A>Title: Sequence homology between human and animal rotavirus serotype-specific glycoprotein
A:Reference number: A93520; MUID:84221410; PMID:6328448
A:Accession: A93520
A:Molecule type: DNA
A:Residues: 1-326 <DVA>
A:Cross-references: GB:X00572; NID:g61680; PIDN:CAA25236.1; PID:g61681
A:Experimental source: serotype 2 strain Hu/Australia/5/7
C:Genetics:
A:Map position: segment 9
C:Superfamily: rotavirus glycoprotein VP7
C:Keywords: coat protein; glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:32-32/Product: glycoprotein VP7 #status predicted <GPV>
F:32-48/Region: hydrophobic #status predicted
F:69,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          8.1%, Score 77; DB 1; Length 326;
Best Local Similarity 22.8%; Pred. No. 12;
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY      26 LMLPCSYVMLEFLC-----SFSWLFIFPLQETAKEPCMCK-----FGPDPXKQM 71
         :|::||::|:~::~|||::|+~~~~~|::||:
Db       10 LTIIISILNVLTIKTINIMDYIIFRPILLALISPVRQNQGMYLPTGSLDAYITN 69
         |||::|||::|:~::~|||::|+~~~~~|::||:
QY      72 ASSEPP-----CV-----NKVSDWKELLLNGLYLVYGQVAPNA---NYNDVAFEEV 115
         ::||::||::|:~::~|||::|+~~~~~|::||:
Db       70 STSGEPFLTSTCLCYPAEAKNRISDDMENTLSQLFTKGMPIGSVYFKQYNINDTFVSV 129
         ::||::||::|:~::~|||::|+~~~~~|::||:
QY      116 --RYKNKDMLQTLNKSIONVGTYELHAGDTIIDIFNSEHQVKNNITYGIILLANP 173
        |::||::||:~::~|||::|+~~~~~|::||:
Db       130 NPQLYCDNVV-----LMKYNTSELDSASELDLIINE-----W----LCNP 167
        |::||::||:~::~|||::|+~~~~~|::||:
QY      174 QPIIS 177
        |||
Db       168 MDIS 171

RESULT 10
Sl1688
tumor necrosis factor alpha precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: Sl1688
R:McGrath, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A>Title: Gene sequence of feline tumor necrosis factor alpha.
A:Reference number: Sl1688; MUID:91016860; PMID:2216740
A:Accession: Sl1688
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MG>
A:Cross-references: UNIPROT:P19101; EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777
C:Genetics:
A:Insertions: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carbonydrate (Ser) (covalent) #status predicted
F:145-177/Dsuulfide Bonds: #status predicted

Query Match          8.0%, Score 76.5; DB 2; Length 233;
Best Local Similarity 20.2%; Pred. No. 9.2;
Matches 50; Conservative 31; Mismatches 54; Indels 113; Gaps 12;

QY      7 ENMPLSHSRTOGAORSSWMKLFCISIVMLEFLCGPSWIIF-----IFQLFTAKEPCMCK 61
         |:|::||::|:~::~|||::|+~~~~~|::||:

```

Db	15	EALEPKAGPGQSGK-----CLCLSLPSFLLVAGATTLE-----CLLH	52
QY	62	FG-----PLPSKQMAS--SEPPCVN-----	80
Db	53	FGVIGPOREELPHGQQLINPLPQTLRSRSRTPSDKVAHVANPFAEGQLQLSRBANAL	112
QY	81	-----KASDMLKLELHONGHLYLYGCV-----APNANY--NDVAFPEVRLYKRMQIC	126
Db	113	LANGVELDNLQAKVSDGILYLYSQVLFTFGGQSPSHVLLTHAISRFPAVSYQKQVLLSA	172
QY	127	LTKNSKIQN-----VGTYELHVGPTID-----LINSSEHOVLKNN	162
Db	173	I--KSPCOREPTEGAEAKKWEPEPIYLGIVFOLEKKGDRLSTEINLPAYLIDFAESGQV----	226
QY	163	TYWGIIIL	170
Db	227	YFGIIAL	233

RESULT 11

A86736

hypothetical protein yjhb [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

CjDate: 23-Mar-2002 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004

CjAccession: A86736

R:Bojlotin, A.; Winkler, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weisenbach, J.; Ehrlich, Genome Res. 11, 731-753, 2001

AjTitle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp

AjReference number: A86625; MUID:21235186; PMID:11337471

AjAccession: A86736

AjStatus: Preliminary

AjMolecule type: DNA

AjResidues: 1-209 <STO>

AjCross-References: UNIPROT:Q9CH50; GB:AE005176; PID:G12723820; PIDN:AAK04987.1; GSPDB:GN

AjExperimental source: strain IL1403

CjGenetics:

AjGene: yjhb

Query Match

Best Local Similarity 8.0%; Score 76; DB 2; Length 209;

Matches 37; Conservative 26; Mismatches 69; Indels 44; Gaps 6;

QY

1 MCLSHLENNPUSHRTQGAQRSSMKMLFCSTIVMLTFLCSFWLIFLQLETAKEPCMA 60 |

Db

33 LALALFTLLARSRASVLRITISFLWAS--VMILFTVGMFWMLAITF----- 78 |

QY

61 KFGPLPSKQVASSBPCKVNVKSDWKLLEILQNGL-YLYGQVAP-----NANVDVAP 112 |

Db

79 -----PTACIVFMKNNPREGGVKNFSDIEDQSESIINERQNDIID 122 |

QY

113 FEVRILYK--NEDMQLTTLNKSRI--QNVGGTYELHVGPTIDLLINSEHOVLKNN 162 |

Db

123 LDDVTFKBSGNSLSIKMTGNTKIIVPEIDVGSLLDTNAGLTKVFEAAQINAGN 178 |

RESULT 12

E70125

hypothetical protein BH0205 - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

CjDate: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004

CjAccession: E70125

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Iathigra, R.; White, son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 350, 580-586, 1997

AjAuthors: Smith, H.O.; Venter, J.C.

AjTitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

AjReference number: AY0100; MUID:98065943; PMID:9403685

AjAccession: E70125

AjStatus: preliminary; nucleic acid sequence not shown; translation not shown

AjMolecule type: DNA

AjResidues: 1-525 <KJL>

AjCross-References: UNIPROT:O51223; GB:AE001131; GB:AE000783; NID:G2688098; PIDN:ACG66601

A;Experimental source: strain B31  
C;Superfamily: *Borrelia burgdorferi* hypothetical protein BB0205

Query Match	8.0%	Score	76	DB	2	Length	525
Best Local Similarity	23.1%	Pred.	No. 27				
Matches	37	Conservative	28	Mismatches	53	Indels	42
						Gaps	7

0Y 44 LIPIFLOETAKE---PCMAKFGLP-----SKWMASESEPCCVNVKSWDKLEI 89  
| : : : : :  
Db 345 LVNIFCIYDTYDELVPILIIKESANPLETYKFILIEGSGATYYRSKRREPKQCTKKKFFDIYM 404

Dd

OY		90	LQNGGLLYLL---	YGQVAP-----	NANYDVAPFEVRLL----	YNKMDI	124
			: :	:	:		
			:	:	:		
			:	:	:		
		405	LENFLTLILAFEDGIVDVKNNKNENNLEFGAAVEEYMSTAPNLSITINKNQTYKIEELII				464

QY 125 QÜITNKS-KIÖNVCGETYELHVGDTID-LIENSEHOVLN 161  
DB 465 MDLENKEILLKQANGNYKKNPLNNVDDPFIKNSLPELKNK 504

RESULT 13  
S51934

MADS-box protein GAIL2 - Norway spruce  
C/Species: Picea abies (Norway spruce)  
C/Date: 14-Jul-1995 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C/Accession: U14477.5S1934  
R/Tandem, K.; Albert, V.A.; Sundas, A.; Engstroem, P.  
Send me, P. 11/27/95

A>Title: Conifer homologues to genes that control floral development in angiosperms  
A|Reference number: S51934; MUID:95170009; PMID:7855797

A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA

A: Cross-references: UNIPROT:Q040766; EMBL:X79280; NID:g695687; PIDN:CAA55867.1; PID:g69566  
A: Experimental source: female cone

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 92-156 <TA2>
```

C:Genetics:  
A:Gene: dal2  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C:Keywords: DNA binding; transcription regulation  
P;2-37;Domain: serum response factor DNA-binding domain homology <SRF>

Query Match	Score	DB 2;	Length
7.9%;	75.5;	DB 2;	Length 222;
Best Local Similarity	30.04;	Best Local	30.04;

DQ 15 RTGSAQRSSMKMLFCSIVMLFLCSPSWLIFILQ-----LETAKPEPC-AKGGPLPS 67  
| : :: | : : : : : : : : : :  
Dd 24 RRNGILLKAYELSVLCDAEVALIVFSSGRGLYEFANHSVKTIRYYKKTCVDNNHGGVIS 83

QY 68 K-----WQASSEPCCVKNKSDWKLEITLONGLYILIGQVAPRANANYDVAPEFRLYKNKD 122

QY	123	M I O T L T N K S K I Q N V G G T Y E L H V G D T I D L I F N S E H Q V L K N N	162
	:::	:::	:::
Db	137	R V R S K N E M L L E E ----- I D I M O R R E H I L I Q E N	164

## RESULT 14

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

Proc. Natl. Acad. Sci. U.S.A. 91, 11065-11069, 1994  
 A1:Title: Major histocompatibility complex class I genes of the coelacanth *Latimeria chalumnae*  
 A1:Reference number: 150810; MIMD:95062206; PMID:7972010

A:Accession: I50811  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Notes: 1. Molecular cloning of human

A:Residues: 1-314 <BET>  
 A:Cross-references: UNIPROT:Q31417; EMBL:U08034; NID:G549857; PIDD:AAA52346.1; PIDD:G560  
 C:Genetic:

A;Gene: Lach-UB-01  
A;Introns: 91/1; 183/1; 276/1

c/superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match	7.9%;	Score	75.5;	DB	2;	Length	314;
Best Local Similarity	34.2%;	Pred. No.	16;				
Matches	26;	Conservative	9;	Mismatches	26;	Indels	15;
						Gaps	5

Qy 55 K E P C M A K G P L P S K M Q M A S E P C V N K S D M K L T L Q N G L - Y L Y I G Q V A P N A N Y N D V A P 112  
 Db 138 K A I R S K V C P V D E A M D S Y F S E - - - D W K Q E I E - G L K K Y L Y L G K - - - E T L E R K V A P 185

```

QY      113 FEVRLYKXKDMIQTLT 128
          |||:| |:|
Db      186 -EVRVYDRPDLERLTL 200

```

RESULT 15  
T20898

hypothetical protein F14F3.2 - *Caenorhabditis elegans*

CiDate: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
CiAccession: T20898

submitted to the EMBL Data Library, June 1995  
A;Reference number: Z19343

A1:Accession: T20898  
A1:Status: preliminary; translated from GB/EMBL/DBJ  
A1:Molecule type: DNA

A; Cross-references: UNIPROT:Q19467  
A; Experimental source: clone F14F3

A;Gene: CESP:F14F3.2  
A;Map position: X

A; Introns: 9/1; 49/1

A; Introns: 9/1; 49/1

A; Introns: 9/1; 49/1

Matches	40;	Conservative	26;	Mismatches	64;	Indels	47;	Gaps	6;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

```
QY      11 LSHERTOGARORSSWKLMFLFCSTVMTLFFLCSPFWLIPIFLOLETAKEPCNAKFGPLESKWQ   70  
       :|::||:          |:::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db     319 MSARNQRKOK-----LAKFTPIQTLLIDLTKDQKRITGDNPA---    35
```

QY 71 MASSEPP-CVNKYSDKLEILONGIYLIYQVA-----PNAVNY----- 106  
||| : : : : :  
Db 360 -PVSEPPNMRKSNDDPLRLIMKSEYADYDEVAGISCSPIGIVPNSQANTLDESSRYW 418

```
QY      109 -DVAPEFVELYKNKDMIQITLNKSKIQNVGTYELHVGDTITLIFNSHQVLKNNTY 164
      :: : || : ||| | : | : : ||| : : : |
Db      419 DELLEMKEKLSSTETMNVLTIK---QNEELTKLVHSLQAVQININSELIITFRDLY 471
```

Search completed: November 2, 2004, 12:41:42  
Job time : 43 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

## OM protein - protein search, using sw model

Run on: November 2, 2004, 11:50:25 ; Search time 154 Seconds

(without alignments)  
412.306 Million cell updates/sec

Title: US-10-080-455-1

Perfect score: 951  
Sequence: 1 MCLSHENPLSHRPTQQAQ.....VLKNTYWGILLANPQFIS 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	100.0	177	2	AAV15817 Amino aci
2	951	100.0	177	2	AAV06646 Human PRO
3	951	100.0	177	4	AAAB47056 PRO175, 5
4	951	100.0	177	4	AAAB20109 Human imm
5	951	100.0	177	4	AAAB53065 Human ang
6	951	100.0	177	4	AAAB47287 PRO175 po
7	951	100.0	177	4	AAAB50979 Human PRO
8	951	100.0	177	5	AAUB1953 Human PRO
9	951	100.0	177	6	ABRA42323 Human GIT
10	951	100.0	177	6	ABP60544 Human tum
11	951	100.0	177	7	ADCC35222 Human TNF
12	951	100.0	177	7	ABW02285 Human end
13	906	95.3	169	3	AAW37847 Human end
14	906	95.3	169	3	AAAB08785 A human e
15	906	95.3	169	3	AAV53061 Human end
16	906	95.3	169	3	AAAB1464 Human end
17	906	95.3	169	7	ADCC01858 Human End
18	566	59.5	508	4	ABG17426 Novel hum
19	281	29.5	52	4	AAAM70748 Human bon
20	85.5	9.0	377	4	AAAM38998 Human pol
21	85.5	9.0	377	5	AAE14752 Human WKL
22	85.5	9.0	377	5	AAE14753 Human WKL
23	85.5	9.0	377	7	ADN38962 Cancer/an
24	85.5	9.0	415	8	ADQ17815 Human sot
25	85.5	9.0	441	4	AAAM41041 Human pol

26	84.5	8.9	1221	7	ADC94332	Adc94332 E. faeciu
27	82	8.6	1188	3	AAAB18183	Aab18183 Plasmodiu
28	81	8.5	162	4	AAU57900	Aau57900 Propionib
29	81	8.5	162	6	ABM54419	Abm54419 Propionib
30	80.5	8.5	107	6	ABM64618	Abm64618 Propionib
31	79.5	8.4	851	5	ABB93512	Abb93512 Herbicida
32	79.5	8.4	879	5	ABP35594	Abp35594 Fungal ZB
33	79	8.3	1013	7	ADB09068	Adb09068 Fungal pro
34	78.5	8.3	599	5	ABP25933	Abp25933 Streptoco
35	78	8.2	105	4	AA62280	Aag62280 Human gen
36	77.5	8.1	226	5	ABBB3970	Abb3970 Human U2
37	77.5	8.1	880	5	ABP35593	Abp35593 Fungal ZB
38	77.5	8.1	3614	4	ABBB62664	Abb62664 Drosophill
39	77	8.1	183	3	AAAG43533	Aag43533 Arabidops
40	77	8.1	228	3	AAAG43532	Aag43532 Arabidops
41	77	8.1	230	3	AAAG43531	Aag43531 Arabidops
42	77	8.1	326	1	AAE60547	Aap60547 Segment 8
43	77	8.1	326	7	ADE36761	Ades36761 Rhesus ro
44	77	8.1	2763	2	AAAM10344	Aam10344 Maize dwa
45	76.5	8.0	1138	5	AAO21502	Aao21502 1138-mer

## ALIGNMENTS

RESULT 1  
AAV15817  
ID AAV15817 standard; protein; 177 AA.

AC AAV15817;  
DT 28-JUL-1999 (first entry)  
XX  
XX  
XX Amino acid sequence of human DNA19355 polypeptide.  
DE  
XX  
XX DNA19355; tumour necrosis factor homologue; receptor GTR; immunogen;  
KW antibody; apoptosis; mammalian cancer cell;  
KW tumour necrosis factor (TNF)-alpha secretion; primary T- cell;  
KW proinflammatory response.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9925834-A1.  
XX  
XX PD 27-MAY-1999.  
XX  
XX PF 18-NOV-1998; 98WO-US024621.  
XX  
XX PR 18-NOV-1997; 97US-0065635P.  
XX  
XX PR 12-DEC-1997; 97US-0069661P.  
XX  
XX PA (GETH ) GENENTECH INC.  
XX  
XX PI Ashkenazi AJ, Gurney AL, Marsters SA, Pitti R, Baker KP;  
PI Godowski PJ, Mark MR;  
XX  
XX WPI: 1999-338009/28.  
XX  
XX N-PSDB; AAX59744.  
XX  
XX PS Claim 10; Fig 1; 86p; English.  
XX  
XX The present sequence represents a polypeptide designated DNA19355. The polypeptide is a tumour necrosis factor homologue. The DNA19355 polynucleotide sequence can be used to derive hybridisation probes for e.g. isolating similar sequences, gene mapping, genetic analysis, etc. Nucleic acids which encode DNA19355 can also be used to generate transgenic or knockout animals, which are useful in the development and screening of therapeutically useful reagents. The DNA19355 polypeptides may be used in diagnostic assays to detect the presence of the receptor GTR in mammalian tissues. The polypeptides can also be used as immunogens to raise antibodies. The polypeptides may also be used to

CC induce apoptosis in mammalian cancer cells. DNA19355 polypeptides  
CC stimulate secretion of tumour necrosis factor (TNF)-alpha in primary T-  
CC cells, and so can be used to stimulate a proinflammatory response in  
CC mammalian cells

XX Sequence 177 AA;

Query Match 100.0%; Score 951; DB 2; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.7e-97;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCGSIYMLLFCFSFSLIFIFLOETAKEPCMA 60  
DB 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCGSIYMLLFCFSFSLIFIFLOETAKEPCMA 60  
QY 61 KFGPLPSKQWASSBPCCVKNKVSQWKLKELIQNGLYLIYQVAPNANNVDAPEEVLTKN 120  
DB 61 KFGPLPSKQWASSBPCCVKNKVSQWKLKELIQNGLYLIYQVAPNANNVDAPEEVLTKN 120  
QY 121 KDMIOQLTNKSKTIQWVGTYELHVGDTIDLINSEHOVLKNNTYGIIILANPOFIS 177  
DB 121 KDMIOQLTNKSKTIQWVGTYELHVGDTIDLINSEHOVLKNNTYGIIILANPOFIS 177

#### RESULT 2

AAV06646  
ID AAV06646 standard; protein; 177 AA.

AC AAV06646;  
DT 26-OCT-1999 (first entry)

DE Human PRO364 ligand.

KM PRO364 ligand; tumour necrosis factor receptor; human; apoptosis;  
KM inflammation; antiinflammatory; NF-KB activation; autoimmune disease;  
KM therapy.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH 1..25  
FT Domain /note= "cytoplasmic domain"  
FT 26..51  
FT Domain /note= "transmembrane domain"  
FT 52..177  
FT Domain /note= "extracellular domain"  
FT Modified-site 129  
FT /note= "N-glycosylation"  
FT Modified-site 161  
FT /note= "N-glycosylation"

XX WO9940196-A1.

XX 12-AUG-1999.

XX 09-FEB-1999; 99WO-US002642.

XX 09-FEB-1998; 98US-0074087P.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Gurney AL, Marsters SA, Pitti RM, Wood WI;  
PI Goddard A;

XX WPI; 1999-494296/41.

XX N-PSDB; AAX87726.

XX Tumor necrosis factor receptor homologue - useful for, e.g. modulating  
PT apoptosis and NF-KB activation and proinflammatory or autoimmune  
PT responses.

XX Example 2; Fig 5A; 104pp; English.

XX The present sequence represents a putative ligand for PRO364 (see also  
CC AAY06605), a novel member of the tumour necrosis factor receptor family.  
CC The sequence was deduced from an isolated cDNA clone (see AAX87726).  
CC Hydrophathy analysis suggests a type II transmembrane homology. The  
CC mol. wt. is 20,308. Identity is shown to human Apo-2L (19.8%), Fas/Apo1-  
CC ligand (19.0%), TNF-alpha (20.6%) and lymphotxin-alpha (17.5%). PRO364  
CC is useful for modulating apoptosis, NF-KB activation and proinflammatory  
CC or autoimmune responses in mammalian cells

XX Sequence 177 AA;

Query Match 100.0%; Score 951; DB 2; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.7e-97;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCGSIYMLLFCFSFSLIFIFLOETAKEPCMA 60  
DB 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCGSIYMLLFCFSFSLIFIFLOETAKEPCMA 60  
QY 61 KFGPLPSKQWASSBPCCVKNKVSQWKLKELIQNGLYLIYQVAPNANNVDAPEEVLTKN 120  
DB 61 KFGPLPSKQWASSBPCCVKNKVSQWKLKELIQNGLYLIYQVAPNANNVDAPEEVLTKN 120  
QY 121 KDMIOQLTNKSKTIQWVGTYELHVGDTIDLINSEHOVLKNNTYGIIILANPOFIS 177  
DB 121 KDMIOQLTNKSKTIQWVGTYELHVGDTIDLINSEHOVLKNNTYGIIILANPOFIS 177

#### RESULT 3

AAB47056  
ID AAB47056 standard; protein; 177 AA.

AC AAB47056;

DT 08-MAY-2001 (first entry)

DE PRO175.

KM PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
KM hGTR; ligand; hGTR; PRO175; tumour necrosis factor receptor; TNFR;  
KM human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
KM myocardial infarction; PGF 2alpha; trauma; cancer; angiogenesis;  
KM age-related macular degeneration; antibody; periodontal disease;  
KM vascular-related drug targeting; atherosclerosis; hypertension;  
KM inflammatory vasculitides; Reynaud's disease; aneurysm;  
KM arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;  
KM fibrosis; neuropathy; rheumatoid arthritis.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH 1..25  
FT Region /note= "Cytoplasmic region"  
FT 26..51  
FT Region /note= "Transmembrane region"  
FT 52..177  
FT Region /note= "Extracellular region"  
FT Modified-site 129  
FT /note= "N-glycosylated"  
FT Modified-site 161  
FT /note= "N-glycosylated"

XX WO200103720-A2.

XX 18-JAN-2001.

XX 11-JUL-2000; 2000WO-US018867.

XX 12-JUL-1999; 99US-014304P.

XX (GETH ) GENENTECH INC.

PI Williams PM, Gerritsen ME;  
 XX  
 DR WPI: 2001-138257/14.  
 DR N-PSDB; AAC85435.  
 XX  
 PT Composition for diagnosing and treating cardiovascular, endothelial and  
 PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.  
 XX  
 PS Claim 2; Fig 5; 76pp; English.  
 XX  
 CC This sequence represents PRO175 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor ligand (IGTR). The  
 CC corresponding receptor (IGTR), PRO364, is given in AAB20109. PRO364 and  
 CC PRO175 may be used in a mixture with a cardiovascular, endothelial,  
 CC angiogenic or angiostatic agent for the treatment of a cardiovascular,  
 CC endothelial, angiogenic or angiostatic disorder. The PRO364 sequence was  
 CC isolated from an expressed sequence tag (EST) database as having homology  
 CC to members of the tumor necrosis factor receptor (TNFR) family of  
 CC polypeptides. The PRO175 CDNA sequence was isolated from a library of  
 CC cDNA fragments derived from human umbilical vein endothelial cells  
 CC (HUVEC). Administering an effective amount of PRO364 or PRO175 or their  
 CC antagonists is useful for treating cardiac hypertrophy (which is  
 CC initiated by myocardial infarction and characterized by the presence of  
 CC an elevated level of PGP 2alpha), trauma, a cancer, or age-related  
 CC macular degeneration in a human. Administering a therapeutically  
 CC effective amount of an antibody that binds PRO364 or PRO175 is useful for  
 CC inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering  
 CC from a tumor or a retinal disorder. PRO364 or PRO175, or their  
 CC antagonists, are useful for vascular-related drug targeting or as  
 CC therapeutic targets for the treatment or prevention of atherosclerosis,  
 CC hypertension, inflammatory vasculitis, Reynaud's disease, aneurysms,  
 CC arterial stenosis, thrombophlebitis, tumor angiogenesis, gut protection  
 CC or regeneration and treatment of lung or liver fibrosis, periodontal  
 CC diseases, attraction of bone-forming cells, central and peripheral  
 CC nervous system disease and neuropathies and rheumatoid arthritis  
 CC  
 XX  
 SQ Sequence 177 AA:  
 Query Match 100.0%; Score 951; DB 4; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 4, 7e-97;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MCLSHENMPLSHSRTOGAQRSSWKLFCISIVALLPFCISFWSLIFLQLETAKEPCMA 60  
 Db 1 MCLSHENMPLSHSRTOGAQRSSWKLFCISIVALLPFCISFWSLIFLQLETAKEPCMA 60  
 Qy 61 KFGPLPSKQWQASSEPCVKNKVDKLEIIQNGIYLYIGOVAPNANTNDVAPFEVRLYKN 120  
 Db 61 KFGPLPSKQWQASSEPCVKNKVDKLEIIQNGIYLYIGOVAPNANTNDVAPFEVRLYKN 120  
 Qy 121 KDMIQTLTNKSKIONVGTVEIHHGDTIIDLFENSEHOVLKNNMTWGIILANPOFIS 177  
 Db 121 KDMIQTLTNKSKIONVGTVEIHHGDTIIDLFENSEHOVLKNNMTWGIILANPOFIS 177  
 RESULT 4  
 AAB20109  
 ID AAB20109 standard; protein; 177 AA.  
 XX  
 AC AAB20109;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Human immunostimulant PRO175.  
 XX  
 KW PRO175; UNQ149; human; immune disease; autoimmune disease; antirheumatic;  
 KW antirheumatic; antiinflammatory; antiinfective; immunosuppressive;  
 KW antitumor; antidiabetic; neuroprotective; hepatoprotective; virucide;  
 KW dermatological; antipsoriatic; antiasthmatic; antiallergic;  
 KW immunostimulant.  
 XX  
 OS Homo sapiens.  
 XX

EH Key Location/Qualifiers  
 FT Peptide 1..44  
 FT Modified-site /label= Signal\_peptide  
 FT Modified-site 18..24  
 FT Protein /note="N-myristoylation site"  
 FT Modified-site 45..177  
 FT Modified-site /label= Mature\_protein  
 FT Modified-site 129..133  
 FT Modified-site /note="Asn is N-glycosylated"  
 FT Modified-site 161..165  
 FT Modified-site /note="Asn is N-glycosylated"  
 XX  
 XX WO200105972-A1.  
 XX  
 XX 25-JAN-2001.  
 XX  
 XX 15-MAR-2000; 2000MO-US006884.  
 XX  
 XX 20-JUL-1999; 99US-0144758P.  
 XX  
 XX (GENTH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ,  
 XX Gurney AJ, Hillan KU, Marx MR, Marsters SA, Pileri RM, Tumas D,  
 XX Matanabe CK, Wood WI;  
 DR WPI: 2001-103149/11.  
 DR N-PSDB; AAF30051.  
 PS Claim 20; Fig 4; 127pp; English.  
 XX  
 CC The present sequence is that of PRO175 (UNQ149), a novel human  
 CC immunomodulator protein (20 kDa, pI 8.08) showing homology to tumor  
 CC necrosis factor family members. The invention provides polynucleotides  
 CC (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)  
 CC including PRO175. Claimed compositions comprising these proteins or their  
 CC agonists are useful for increasing infiltration of inflammatory cells  
 CC into a tissue of a mammal, stimulating or enhancing an immune response in  
 CC a mammal, or increasing the proliferation of T-lymphocytes in a mammal in  
 CC response to an antigen. Claimed compositions comprising the PRO  
 CC polypeptide or its antagonist have the opposite effect. A claimed method  
 CC for treating an immune related disorder, such as a T cell disorder,  
 CC involves administering the PRO polypeptide, an agonist antibody or an  
 CC antagonist antibody. The disorder is selected from systemic lupus  
 CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic  
 CC arthritis, spondyloarthritis, systemic sclerosis, idiopathic  
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,  
 CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia,  
 CC thyroditis, diabetes mellitus, immune-mediated renal disease,  
 CC demyelinated diseases (such as multiple sclerosis), autoimmune chronic  
 CC active hepatitis, primary biliary cirrhosis, granulomatous hepatitis,  
 CC sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis  
 CC and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease,  
 CC (auto)immune-mediated skin diseases (such as bullous skin disease,  
 CC erythema multiforme and psoriasis), allergic diseases (such as asthma,  
 CC allergic rhinitis, atopic dermatitis, food hypersensitivity and  
 CC urticaria), immunologic diseases of the lung and transplantation  
 CC associated diseases (such as graft rejection and graft-versus-host  
 CC disease) (all claimed). Claimed methods of diagnosing these disorders  
 CC comprise detecting the level of expression of the PRO gene. Also claimed  
 CC are a method of identifying a compound capable of inhibiting the  
 CC expression or activity of the PRO polypeptide, vectors, host cells,  
 CC antibodies, and a method of stimulating an immune response in a mammal  
 CC using PRO179  
 XX  
 SQ Sequence 177 AA:  
 Query Match 100.0%; Score 951; DB 4; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 4, 7e-97;

Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPHSHSTQGAQRSSMKLMLFCSTVMLLFLCSFWMLFIPLQETAKEPCMA 60  
 DB 1 MCLSHLEMPHSHSTQGAQRSSMKLMLFCSTVMLLFLCSFWMLFIPLQETAKEPCMA 60  
 QY 61 KFGPLPSKQMASSSEPPCVNKNVSDMKLELLQNGLYLIYGQVAPNANNYDVAFFEVRLYKN 120  
 DB 61 KFGPLPSKQMASSSEPPCVNKNVSDMKLELLQNGLYLIYGQVAPNANNYDVAFFEVRLYKN 120  
 QY 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLIFNSEHQVLKNNTWGIIILANPQFIS 177  
 DB 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLIFNSEHQVLKNNTWGIIILANPQFIS 177

RESULT 5  
 AAB53065  
 ID AAB53065 standard; protein, 177 AA.  
 XX AAB53065;  
 AC  
 XX 28-FEB-2001 (first entry)  
 DT  
 XX Human angiogenesis-associated protein PRO175, SEQ ID NO:9.  
 DE Human angiogenesis-associated protein; PRO; endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053753-A2.  
 XX  
 PD 14-SEP-2000.  
 PF 05-JAN-2000; 2000WO-US000219.  
 XX  
 XX 08-MAR-1999; 99WO-US005028.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144738P.  
 PR 26-JUL-1999; 99WO-US020111.  
 PR 01-SEP-1999; 99WO-US020594.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 30-NOV-1999; 99WO-US028409.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Garber H, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pillel RM, Watanabe CK, Williams PM, Wood WJ;  
 XX WPI; 2001-090793/10.  
 DR N-PSDB; AAC97374.  
 XX  
 PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic  
 PT disorders, such as atherosclerosis, wounds or cancer.  
 XX  
 PS Claim 69, Fig 4, 293pp; English.

CC The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity; diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
 CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO  
 CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to screen  
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map  
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene  
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals  
 CC useful for the development and screening of potential therapeutic agents.  
 CC The present sequence represents a PRO protein of the invention  
 XX

Sequence 177 AA;

Query Match 100.0%; Score 951; DB 4; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-97;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPHSHSTQGAQRSSMKLMLFCSTVMLLFLCSFWMLFIPLQETAKEPCMA 60  
 DB 1 MCLSHLEMPHSHSTQGAQRSSMKLMLFCSTVMLLFLCSFWMLFIPLQETAKEPCMA 60  
 QY 61 KFGPLPSKQMASSSEPPCVNKNVSDMKLELLQNGLYLIYGQVAPNANNYDVAFFEVRLYKN 120  
 DB 61 KFGPLPSKQMASSSEPPCVNKNVSDMKLELLQNGLYLIYGQVAPNANNYDVAFFEVRLYKN 120  
 QY 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLIFNSEHQVLKNNTWGIIILANPQFIS 177  
 DB 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLIFNSEHQVLKNNTWGIIILANPQFIS 177

RESULT 6  
 AAB47287  
 ID AAB47287 standard; protein, 177 AA.  
 XX AAB47287;  
 AC  
 XX 22-AUG-2001 (first entry)  
 DT  
 XX PRO175 polypeptide.  
 DE  
 XX  
 XX PRO; type II transmembrane protein; tumour necrosis factor; stroke;  
 KW heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;  
 KW myocardial infarction; cardiac hypertrophy; PGF 2alpha; trauma; bone;  
 KW cancer; age-related macular degeneration; wound; burn; hypertension;  
 KW diabetes mellitus; osteoporosis; ischaemia; atherosclerosis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; amyloidotic lateral sclerosis;  
 KW endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX Peptide 1..25



FT	Modified-site	/label= Signal peptide
FT		18. .24
FT	Protein	/label= N-myristoylation site
FT		26. .177
FT	Domain	/label= Mature PRO175
FT		26. .51
FT	Domain	/label= Transmembrane domain
FT		52. .177
FT	Modified-site	/label= Extracellular domain
FT		129. .133
FT	Modified-site	/label= N-linked glycosylation site
FT		161. .165
FT	Modified-site	/label= N-linked glycosylation site
XX		
PN	WO200140464-A1.	
XX		
PD	07--JUN-2001.	
XX		
PE	11-AUG-2000; 2000WO-US022031.	
XX		
PR	30-NOV-1999; 99WO-US028313.	
PR	30-NOV-1999; 99WO-US028409.	
PR	05-JAN-2000; 2000WO-US000219.	
PR	24-FEB-2000; 2000WO-US005004.	
PR	15-MAR-2000; 2000WO-US006884.	
PR	30-MAR-2000; 2000WO-US008439.	
PR	17-MAY-2000; 2000WO-US013705.	
PR	30-MAY-2000; 2000WO-US014941.	
PR	28-JUL-2000; 2000WO-US020710.	
XX		
PA	(GERTH ) GENENTECH INC.	
PI	Askenazi AJ, Baker KP, Ferrara N, Godowski PJ, Gurney AL;	
PI	Hillan KJ, Mark MR, Marsters SA, Paoni NF, Piltti RM, Wood WI;	
XX		
DR	WPI; 2001-381383/40.	
DR	N-PSDB; AAC85945.	
XX		
PS	Claim 56; Fig 2; 144dp; English.	
XX		
CC	The sequences given in AAs47287-90 show PRO polypeptides. PRO175 shows	
CC	type II transmembrane protein typology, and portions of PRO364 show	
CC	homology to members of the tumour necrosis factor (TNF) family, thereby	
CC	indicating that it may be a novel member of the TNF family. PRO175 and	
CC	PRO185 stimulated heart hypertrophy. PRO cDNA's may be used to identify a	
CC	compound that inhibits PRO, diagnosing a cardio-vascular, endothelial or	
CC	angiogenic disorder in a mammal by detecting PRO cDNA, treating	
CC	cardiovascular, endothelial or angiogenic disorder in a mammal, and	
CC	inducing cardiac hypertrophy or inhibiting endothelial cell growth or	
CC	angiogenesis in a mammal. The mammal is a human which has suffered	
CC	myocardial infarction, cardiac hypertrophy characterized by the presence	
CC	of elevated BGF, xalpa, trauma, cancer or age-related macular	
CC	degeneration. Trauma includes wounds or burns. Other treatable diseases	
CC	include diabetes mellitus, osteoporosis, ischaemia, hyper-tension,	
CC	rheumatoid arthritis, Crohn's disease, atherosclerosis, psoriasis,	
CC	endometriosis, angina, neoplasms, periodontal disease, bone and cartilage	
CC	repair, Alzheimer's disease, neoplasms, Parkinson's disease, Huntington's disease,	
XX	amyotrophic lateral sclerosis, and stroke	
XX	Sequence 177 AA;	

	Query Match	100.0%	Score 951;	DB 47	Length 177;
	Best Local Similarity	100.0%	Pred. No. 4,7e-97;		
	Matches	177;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	1	MCLSLHEMPSPHSHSTQGAQRSSWKLTMFCGSIYVLLFFICPSFWMLFIPILOLETKAPEPCMA			60
DB	1	MCLSLHEMPSPHSHSTQGAQRSSWKLTMFCGSIYVLLFFICPSFWMLFIPILOLETKAPEPCMA			60

Cy	61	KFGPLPSKQWMASSPEPCNVKISDWKLEHLNGLYLIYGVAPNANVDVAFEVRLYKN	120
	61	KFGPLPSKQWMASSPEPCNVKISDWKLEHLNGLYLIYGVAPNANVDVAFEVRLYKN	120
Db	61	KFGPLPSKQWMASSPEPCNVKISDWKLEHLNGLYLIYGVAPNANVDVAFEVRLYKN	120
Cy	121	KDMLQTLTKSKSIQNVGYTEYHLVADTLDLFNSHQVLKNNITYGIIILANPQFIS	177
	121	KDMLQTLTKSKSIQNVGYTEYHLVADTLDLFNSHQVLKNNITYGIIILANPQFIS	177
Db	121	KDMLQTLTKSKSIQNVGYTEYHLVADTLDLFNSHQVLKNNITYGIIILANPQFIS	177
RESULT 7			
ID	AAB50979	standard; protein; 177 AA.	
XX	AA		
XX	AC		
XX	AA		
XX	DT	21-MAR-2001 (first entry)	
XX	DE		
XX	XX	Human PRO175 protein.	
XX	XX		
XX	KW	Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;	
XX	KW	vasotropic; antirheumatic; antiarthritic; antiinflammatory; cystostatic;	
XX	KW	vulnerable; antiangiinal; gene therapy; cardiovascular disease;	
XX	KM	endothelial disorder; angiogenic disorder; cancer; periodontal disease;	
XX	KW	wound healing.	
XX	XX		
OS		Homo sapiens.	
XX	XX		
XX	XX	WO200073445-A2.	
XX	PD		
XX	XX	07-DEC-2000.	
XX	XX		
XX	PF	17-MAY-2000; 2000WO-US013705.	
XX	XX		
XX	PR	02-JUN-1999; 99WO-US012252.	
XX	PR	23-JUN-1999; 99US-0141037P.	
XX	PR	20-JUL-1999; 99US-0144758P.	
XX	PR	26-JUL-1999; 99US-0145698P.	
XX	PR	28-JUL-1999; 99US-0146222P.	
XX	PR	01-SEP-1999; 99WO-US020121.	
XX	PR	30-NOV-1999; 99WO-US028313.	
XX	PR	30-NOV-1999; 99WO-US028409.	
XX	PR	02-DEC-1999; 99WO-US028565.	
XX	PR	16-DEC-1999; 99WO-US030095.	
XX	PR	05-JAN-2000; 2000WO-US000219.	
XX	PR	06-JAN-2000; 2000WO-US000376.	
XX	PR	11-FEB-2000; 2000WO-US003565.	
XX	PR	18-FEB-2000; 2000WO-US004341.	
XX	PR	18-FEB-2000; 2000WO-US004342.	
XX	PR	24-FEB-2000; 2000WO-US005004.	
XX	PR	02-MAR-2000; 2000WO-US005841.	
XX	PR	10-MAR-2000; 2000WO-US006319.	
XX	PR	15-MAR-2000; 2000WO-US006884.	
XX	PR	21-MAR-2000; 2000WO-US007532.	
XX	PR	30-MAR-2000; 2000WO-US008439.	
XX	XX		
PA	(GETH )	GENENTECH INC.	
XX			
PI	Ashtkenazi AJ, Baker KP, Ferrara N, Gerber H, Gertlsen MB;		
PI	Goddard A, Goddowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;		
PI	Paoni NF, Pelti RM, Watanabe CK, Williams PM, Wood WI;		
XX	XX		
DR	XX	WPI; 2001-025251/03.	
XX	XX	N-PSDB; AAC90563.	
XX	XX		
PT	Seventeen nucleic acids encoding PRO polypeptides which are useful in		
PT	diagnosis and treatment of cardiovascular, endothelial or angiogenic		
PT	disorders in a mammal.		
XX	XX		
PS	Claim 71; Fig 2; 182pp; English.		
XX	XX		
CC	The present sequence is one of seventeen novel PRO polypeptides. The PRO		
CC	nucleic acids, polypeptides, agonists and antagonists are useful for		
CC	treating cardiovascular, endothelial or angiogenic disorders in a mammal		

```
CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,
CC age-related macular degeneration, atherosclerosis, hypertension, arterial
CC retinosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial
CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and
CC antagonists are also used to prevent tumour angiogenesis and for treating
CC periodontal diseases. They are also used to stimulate wound healing and
CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO
CC antibodies are useful for diagnosing a cardiovascular, endothelial or
CC angiogenic disorder
XX
SQ Sequence 177 AA;
Query Match 100.0%; Score 951; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.7e-97;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCLSHLEMPLSHRTQAGRSSWKLWLFCSIVMLLFICSFSLFIFLOLETAKPCMA 60
DB 1 MCLSHLEMPLSHRTQAGRSSWKLWLFCSIVMLLFICSFSLFIFLOLETAKPCMA 60
QY 61 KFGPLPSKQWASSSEPPCVNKSVDKLEILLQNGLYLIGQVAPNANYNDVAPFEVRLYKN 120
DB 61 KFGPLPSKQWASSSEPPCVNKSVDKLEILLQNGLYLIGQVAPNANYNDVAPFEVRLYKN 120
QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSHSHQVLKNNYWGIIILANPQFIS 177
DB 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSHSHQVLKNNYWGIIILANPQFIS 177
RESULT 8
AAU81953
ID AAU81953 standard; protein, 177 AA.
XX
AC AAU81953;
XX
DT 09-APR-2002 (first entry)
XX
DB Human PRO175.
XX
KW Human; PRO; antiinflammatory; ophthalmological; vasotropic;
KW retinal cell injury; ocular disease; retinitis pigmentosa;
KW macular degeneration; retinal detachment; retinal tear; retinopathy;
KW retinal degenerative disease; macular hole; degenerative myopia;
KW acute retinal necrosis syndrome; traumatic chorioretinopathy;
KW Putscher's retinopathy; oedema; ischaemic condition;
KW retinal vision occlusion; collagen vascular disease;
KW thrombocytopenic purpura, uveitis; retinal vasculitis; Eales disease;
KW systemic lupus erythematosus; environmental trauma.
XX
OS Homo sapiens.
XX
MOZ00109327-A2.
XX
PD 08-FEB-2001.
XX
PE 28-JUL-2000; 2000WO-US020710.
XX
PR 28-JUL-1999; 99US-0146222P.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021050.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 04-FEB-2000; 2000WO-US005004.
PR 15-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
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XX
PA (GERTH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;
PI Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Pilti RM, Watanabe CK;
PI Wood WJ;
XX
DR MPI: 2002-130120/17.
DR N-PEDB; ABK26562.
XX
PT Promoting survival of retinal cells, or delaying or preventing retinal
PT cell injury or death, by contacting retinal cells with PRO175, 220, 216,
PT 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132 polypeptide.
XX
PS Claim 44; Fig 2; 152pp; English.
XX
DB The invention relates to promoting the survival of retinal cells, or
DB delaying or preventing retinal cell injury or death, by contacting the
DB retinal cells with the polypeptide such as PRO175, PRO220, PRO216,
DB PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,
DB PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids
DB encoding the PRO proteins, a vector comprising the nucleic acid, a host
DB cell comprising the vector, and anti-PRO antibody. The PRO proteins are
DB useful for promoting survival of retinal cells (retinal neurons such as
DB retinal ganglion cells, displaced retinal ganglion cells, amacrine cells,
DB displaced amacrine cells, horizontal neurons or bipolar neurons, rod
DB photoreceptors, or supportive cells such as Muller cells or pigment
DB epithelial cells), or delaying or preventing retinal cell injury or death
DB caused by ocular disease (which is or is associated with retinitis
DB pigmentosa, macular degeneration, retinal detachment, retinal tear,
DB retinopathy, retinal degenerative disease, macular hole, degenerative
DB myopia, acute retinal necrosis syndrome, traumatic chorioretinopathy or
DB contusion, Putscher's retinopathy, oedema, an ischaemic condition,
DB central or branch retinal vision occlusion, collagen vascular disease,
DB thrombocytopenic purpura, uveitis, retinal vasculitis, occlusion
DB associated with Eales disease or systemic lupus erythematosus), retinal
DB injury or environmental trauma. The retinal cell injury or death is
DB delayed or prevented by substantially not causing angiogenesis or
DB mitogenesis. The present sequence represents a PRO protein
XX
SQ Sequence 177 AA;
Query Match 100.0%; Score 951; DB 5; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.7e-97;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCLSHLEMPLSHRTQAGRSSWKLWLFCSIVMLLFICSFSLFIFLOLETAKPCMA 60
DB 1 MCLSHLEMPLSHRTQAGRSSWKLWLFCSIVMLLFICSFSLFIFLOLETAKPCMA 60
QY 61 KFGPLPSKQWASSSEPPCVNKSVDKLEILLQNGLYLIGQVAPNANYNDVAPFEVRLYKN 120
DB 61 KFGPLPSKQWASSSEPPCVNKSVDKLEILLQNGLYLIGQVAPNANYNDVAPFEVRLYKN 120
QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSHSHQVLKNNYWGIIILANPQFIS 177
DB 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSHSHQVLKNNYWGIIILANPQFIS 177
RESULT 9
ABR42323
ID ABR42323 standard; protein, 177 AA.
XX
AC ABR42323;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human GTRPL protein.
XX
KW Human; GTRPL; tumour necrosis factor; ligand; cytostatic;
KW immunomodulator; osteopathic.
XX
OS Homo sapiens.
```



DT 18-DEC-2003 (first entry)  
XX  
DE Human TNF ligand family member #20.  
XX  
KW human; tumour necrosis factor; TNF ligand; endokine alpha;  
XX excessive bone resorption disorder; osteoporosis; Paget's disease;  
XX arterial calcification.  
XX  
OS Homo sapiens.  
XX  
EN US2003100074-A1.  
XX  
PD 29-MAY-2003.  
XX  
PF 15-AUG-2002; 2002US-00218547.  
XX  
PR 16-AUG-2001; 2001US-0312542P.  
XX 30-OCT-2001; 2001US-0330761P.  
XX  
PA (YUGG/) YU G.  
XX (NIJ/) NI J.  
XX (ROSE/) ROSEN C A.  
XX (NARD/) NARDELLI B.  
XX  
PI Yu G, Ni J, Rosen CA, Nardelli B;  
XX  
XX MPI; 2003-696072/66.  
XX N-PSDB; ADC35221.  
XX  
XX  
PT New Endokine alpha gene useful for preparing a composition for treating a  
PT disease associated with excessive or insufficient bone resorption e.g.,  
PT osteoporosis, Paget's disease or arterial calcification.  
XX  
PS Claim 1; SEQ ID NO 40; 145PP; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule encoding a  
CC tumour necrosis factor family ligand. A composition comprising the  
CC isolated antibody or its fragment is used for treating an individual in  
CC need of decreased level of endokine alpha activity. The endokine alpha  
CC polypeptide present in a heterotrimeric complex is used for treating an  
CC individual having a disorder associated with excessive bone resorption,  
CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an  
CC individual having a disorder associated with insufficient bone resorption  
CC comprises administering an endokine alpha antagonist, which is the  
CC antibody that binds specifically to endokine alpha polypeptide. The  
CC present sequence represents the amino acid sequence of a tumour necrosis  
CC factor family ligand.  
XX  
SQ Sequence 177 AA;  
XX  
Query Match 100.0%; Score 951; DB 7; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.7e-97;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLWLFCSIVMLFLCFSFWLFIPLQJETAKEPCMA 60  
DB 1 MCLSHLENMPLSHSRTOGAQRSSWKLWLFCSIVMLFLCFSFWLFIPLQJETAKEPCMA 60  
XX  
QY 61 KFGPLPSKQWASSPSPCVNVSDMKLEILONGYLITYGQVAPNANNVDVAPFEVRLTKN 120  
DB 61 KFGPLPSKQWASSPSPCVNVSDMKLEILONGYLITYGQVAPNANNVDVAPFEVRLTKN 120  
XX  
QY 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLI FNSHQVLYKNTYWGIIILANPQFIS 177  
DB 121 KDMIQTLTNKSKIQNVGTYELHVGDTIDLI FNSHQVLYKNTYWGIIILANPQFIS 177  
XX  
RESULT 12  
ABW02285 standard; protein; 177 AA.  
XX  
AC ABW02285;  
XX

DT 12-FEB-2004 (first entry)  
XX  
DE Human endokine alpha protein.  
XX  
KW Gastrointestinal tract disorder; tumour necrosis factor; TNF; DR3; TR6;  
XX TNF-gamma-beta protein; inflammatory bowel disease; Crohn's disease;  
XX ulcerative colitis; endokine alpha protein; human.  
XX  
OS Homo sapiens.  
XX  
EN US2003198640-A1.  
XX  
PD 23-OCT-2003.  
XX  
PF 06-DEC-2002; 2002US-00310793.  
XX  
PR 07-NOV-1994; 94WO-US012880.  
XX 05-JUN-1995; 95US-00461246.  
XX 09-JAN-1998; 98US-00005020.  
XX 09-FEB-1998; 98US-0074047P.  
XX 07-AUG-1998; 98US-00131237.  
XX 08-FEB-1999; 99US-00246129.  
XX 30-APR-1999; 99US-0131963P.  
XX 03-MAY-1999; 99US-0132227P.  
XX 13-MAY-1999; 99US-0134067P.  
XX 08-FEB-2000; 2000US-0180908P.  
XX 27-APR-2000; 2000US-00559290.  
XX 07-JUL-2000; 2000US-0216879P.  
XX 26-MAR-2001; 2001US-0278449P.  
XX 06-JUL-2001; 2001US-00899059.  
XX 24-AUG-2001; 2001US-0314381P.  
XX 07-DEC-2001; 2001US-0336695P.  
XX 23-AUG-2002; 2002US-00226294.  
XX  
XX (HUMA-) HUMAN GENOME SCT INC.  
XX  
XX Yu G, Ni J, Rosen CA, Zhang J, Wei P;  
PI  
XX MPI; 2003-852773/79.  
XX N-PSDB; AAD63921.  
XX  
XX  
XX Use of tumor necrosis factor gamma-beta antagonists for treating or  
PT ameliorating a disease or disorders of the gastrointestinal tract, e.g.  
PT inflammatory bowel disease, Crohn's disease or ulcerative colitis.  
XX  
XX Disclosure; Page 153-154; 0pp; English.  
XX  
XX  
XX The invention relates to methods and compositions for treating or  
CC ameliorating a disease or disorder of the gastrointestinal tract. The  
CC method involves administering a composition comprising tumour necrosis  
CC factor (TNF)-gamma-beta and its receptors DR3 and TR6 to a person with,  
CC or suspected of having the disease or disorder. The antagonist of TNF-  
CC gamma-beta is useful for treating or ameliorating a gastrointestinal  
CC tract disease or disorder, specifically an inflammatory bowel disease,  
CC e.g. Crohn's disease or ulcerative colitis. The present sequence is human  
CC endokine alpha protein. This sequence is used to illustrate the method of  
CC the invention.  
XX  
SQ Sequence 177 AA;  
XX  
Query Match 100.0%; Score 951; DB 7; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.7e-97;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 13
AAW37847
ID AAW37847 standard; protein; 169 AA.
XX
XX AAW37847;
AC
XX
XX 28-AUG-1998 (first entry)
DT
XX
XX Human endokine-alpha.
DE
XX Endokine-alpha; cytokine; tumour necrosis factor; human;
XX immunomodulation; infection; cell proliferation; angiogenesis; tumour;
XX metastasis; apoptosis; sepsis; endotoxaemia; melanoma; sarcoma;
XX diagnosis; therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 1..17
FT /note= "intracellular domain"
FT 18..43
FT Domain /note= "transmembrane domain"
FT /note= "extracellular domain"
FT /note= "extracellular domain"
FT Peptide 44..158
FT /note= "epitope-bearing fragment (Claim 13)"
FT 44..54
FT /note= "epitope-bearing fragment (Claim 13)"
FT 57..68
FT /note= "epitope-bearing fragment (Claim 13)"
FT Peptide 69..78
FT /note= "epitope-bearing fragment (Claim 13)"
FT 94..105
FT /note= "epitope-bearing fragment (Claim 13)"
FT 108..132
FT /note= "epitope-bearing fragment (Claim 13)"
FT 142..158
FT /note= "epitope-bearing fragment (Claim 13)"
FT Peptide
PN MO9807880-A1.
XX
XX 26-FEB-1998.
XX
XX 16-AUG-1996; 96WO-US013282.
XX
XX 16-AUG-1996; 96WO-US013282.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Yu G, Ni J, Rosen CA;
XX
XX WPI; 1998-169182/15.
XX
XX N-PSDB; AAV19195.
XX
XX Nucleic acid encoding human endokine-alpha - useful for diagnosis and
XX treatment of tumour necrosis factor-related diseases.
XX
XX Claim 1; Fig 1A-B; 78pp; English.
XX
XX This polypeptide comprises human endokine-alpha, a novel member of the
XX tumour necrosis factor (TNF) family of cytokines that shows 30%
XX similarity and 22% identity to human TNF-alpha. Its amino acid sequence
XX was deduced from a human stratum CDNA clone (see AAV19195). Isolation of
XX this nucleic acid allows production of recombinant endokine-alpha
XX polypeptides in transformed host cells. Endokine-alpha may be involved in
XX disorders of immunomodulation, infection, cell proliferation,
XX angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxaemia, and
XX may be useful for treating melanoma and sarcoma, particularly where
XX coupled to a radioisotope or cytostatic agent. Antibodies raised against
```

CC endokine-alpha are useful diagnostically and for treatment of TNF-  
CC associated disease  
XX  
XX Sequence 169 AA;

Query Match 95.3%; Score 906; DB 2; Length 169;  
Best Local Similarity 100.0%; Pred. No. 4.4e-92;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MPELSHRTGAGRSSWKMLFCSYVWLLFLCSTSWILFTFLQETAKEPEPMATGRLPSK 60
QY 69 WQWASSEPCVNVKSPWKLKLEILONGLYLYGQVAPNANVNDVAPFVRLYKXNDMIQTLT 128
DB 61 WQWASSEPCVNVKSPWKLKLEILONGLYLYGQVAPNANVNDVAPFVRLYKXNDMIQTLT 120
QY 129 NRSKIQNVGTVELHVGDTIDILFNSEHQVLKNNYWGIIILANPQFIS 177
DB 121 NRSKIQNVGTVELHVGDTIDILFNSEHQVLKNNYWGIIILANPQFIS 169
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RESULT 14
AAB08785
ID AAB08785 standard; protein; 169 AA.
XX
XX AAB08785;
AC
XX
XX 02-JAN-2001 (first entry)
DT
XX
XX A human endokine-alpha polypeptide.
DE
XX
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Human; endokine-alpha; cytokine; tumour necrosis factor; TNF; AIDS;  
chronic lymphocyte disorder; tumour; parasitic disease; arthritis;  
autoimmune disease; lupus; multiple sclerosis; chronic inflammation;  
acute inflammation; acute allograft rejection; graft versus host disease;  
transplant rejection; foetal resorption; faecal peritonitis; allergy;  
bowel disease; sepsis; leukaemia; chronic hypergammaglobulinaemia;  
polychondritis; scleroderma; Wegener granulomatosis; dermatomyositis;  
chronic active hepatitis; myasthenia gravis; psoriasis; vitiligo;  
Steven-Johnson syndrome; idiopathic spine; gluten-sensitive enteropathy;  
pemphigus vulgaris; Goodpasture's disease; bullous pemphigoid;  
discoïd lupus; dense deposit disease; endocrine ophthalmopathy;  
irritable bowel disease; asthma; Grave's disease; sarcoidosis; cirrhosis;  
juvenile diabetes; insulin dependent diabetes mellitus; uveitis;  
lymphopneumias; polyarteritis nodosa; Sjogren's syndrome; Bechet's disease;  
primary myxedema; polymyositis; mixed connective tissue disease;  
keratoconjunctivitis sicca; vernal keratoconjunctivitis; ss.

```
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 1..17
FT /note= "intracellular domain"
FT 18..43
FT Domain /note= "transmembrane domain"
FT /note= "extracellular domain"
FT Domain
PN WO200050620-A2.
XX
XX 31-AUG-2000.
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XX 25-FEB-2000; 2000MO-US004722.
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XX 26-FEB-1999; 99US-0122099P.
XX
XX 28-MAY-1999; 99US-0136788P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Yu G, Ni J, Rosen CA;
XX
XX WPI; 2000-572097/53.
XX
XX
```

```
DR N-PSDB; AAA74936.
XX
XX Polynucleotide encoding endokine alpha protein, which is a member of
PT tumor necrosis factor useful for treating inflammatory diseases,
PT disorders such as cancer, allergy, diabetes and various neurological
PT disorders.
XX
XX Claim 16; Fig 1; 263pp; English.
XX
XX The present sequence represents a human endokine-alpha polypeptide. The
CC polypeptide is a cytokine which is similar to tumour necrosis factor
CC (TNF). The endokine-alpha polynucleotides and polypeptides are useful for
CC treating AIDS, chronic lymphocyte disorder, tumours, parasitic disease,
CC autoimmune disease, lupus, arthritis, multiple sclerosis, chronic
CC inflammation, acute inflammation, acute allograft rejection, graft versus
CC host disease, transplant rejection, foetal resorption, faecal
CC peritonitis, skin allergies, bowel disease, sepsis, leukaemia, chronic
CC hypergammaglobulinemia, polychondritis, scleroderma, Wegener
CC granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia
CC gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, vitiligo,
CC gluten-sensitive enteropathy, pemphigus vulgaris, Goodpasture's disease,
CC bullous pemphigoid, discoid lupus, dense deposit disease, endocrine
CC opthalmopathy, irritable bowel disease, asthma, Grave's disease,
CC sarcoidosis, cirrhosis, juvenile diabetes, insulin dependent diabetes
CC mellitus, uveitis, lymphopenias, polyarteritis nodosa, Sjogren's
CC syndrome, Bechet's disease, primary myxedema, polymyositis, mixed
CC connective tissue disease, keratoconjunctivitis sicca, and vernal
CC keratoconjunctivitis.
XX
XX Sequence 169 AA;
SQ
Query Match 95.3%; Score 906; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. No. 4.4e-99;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFFLQLETAKEPCMAKFGPLPSK 60
QY 69 WOMASSEPPCVNKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVRLYNKDMIQTLT 128
DB 61 WOMASSEPPCVNKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVRLYNKDMIQTLT 120
QY 129 NKSKIQNVGTYELHVGDTIDLIENSEHQVLKNNTYWGIILLANQFIS 177
DB 121 NKSKIQNVGTYELHVGDTIDLIENSEHQVLKNNTYWGIILLANQFIS 169
RESULT 15
AA53061
ID AA53061 standard; protein; 169 AA.
XX
XX AA53061;
AC
XX
XX 03-APR-2000 (first entry)
DT
XX
XX Human endokine alpha protein SEQ ID NO:2.
DE
XX
XX Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
KM immunomodulation; inflammation; cell proliferation; angiogenesis;
KM tumour metastasis; apoptosis; sepsis; endotoxemia.
XX
XX Homo sapiens.
OS
XX
XX US5998171-A.
PN
XX
XX 07-DEC-1999.
PD
XX
XX 15-AUG-1997; 97US-00912227.
PF
XX
XX 16-AUG-1996; 96US-0024058P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
```

```
XX
XX Ni J, Rosen CA, Yu G;
PI
XX
XX WPI; 2000-104608/09.
DR
XX
XX N-PSDB; AA257314.
DR
XX
XX Isolated human endokine alpha gene useful as a diagnostic probes and
PT primers.
PT
XX
XX Claim 1; Fig 1; 31pp; English.
PS
XX
XX The present sequence represents human endokine alpha which is a member of
CC the tumour necrosis factor (TNF) family of cytokines. Endokine alpha
CC protein and polynucleotides can be used in diagnostic and therapeutic
CC methods concerning TNF family-related disorders. These include disorders
CC associated with immunomodulation and inflammation, cell proliferation,
CC angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxemia
XX
XX Sequence 169 AA;
SQ
Query Match 95.3%; Score 906; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. No. 4.4e-92;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MPLSHSRTOGAQRSSWKMLFCSIVMLFLCFSFWLIFFLQLETAKEPCMAKFGPLPSK 60
QY 69 WOMASSEPPCVNKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVRLYNKDMIQTLT 128
DB 61 WOMASSEPPCVNKVSDWKLLEILQNGLYLIYGQVAPNANYNDVAPPEVRLYNKDMIQTLT 120
QY 129 NKSKIQNVGTYELHVGDTIDLIENSEHQVLKNNTYWGIILLANQFIS 177
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Search completed: November 2, 2004, 12:37:39
Job time : 159 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2004, 12:41:06 ; Search time 129 Seconds  
(without alignments)  
444.854 Million cell updates/sec

Title: US-10-080-455-1

Perfect score: 951

Sequence: 1 MCLSHLENNPLSHSRTOGA.....VLKNNYWGILLANPQFIS 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.\*  
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2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	100.0	177	13	US-10-080-455-1
2	951	100.0	177	13	US-10-116-378-16
3	951	100.0	177	14	US-10-151-882-39
4	951	100.0	177	14	US-10-218-547-40
5	951	100.0	177	14	US-10-310-793-44
6	951	100.0	177	14	US-10-310-793-44
7	906	95.3	169	9	US-09-345-790-2
8	906	95.3	169	13	US-10-136-511-2
9	608	63.9	113	14	US-10-338-083-17
10	608	63.9	113	16	US-10-611-399-17
11	281	29.5	52	9	US-09-864-761-48455
12	85.5	9.0	377	14	US-10-295-027-280
13	79.5	8.4	246	15	US-10-424-599-201262

14	79.5	8.4	879	15	US-10-149-310-52	Sequence 52, Appl
15	77.5	8.1	880	15	US-10-149-310-50	Sequence 50, Appl
16	76.5	8.0	1138	14	US-10-261-482-4	Sequence 4, Appl
17	76	8.0	1133	16	US-10-437-963-149870	Sequence 149870,
18	75.5	7.9	365	15	US-10-425-114-47601	Sequence 47601, A
19	75.5	7.9	885	16	US-10-432-171-12	Sequence 12, Appl
20	75.5	7.9	5795	9	US-09-815-242-12610	Sequence 12610, A
21	74.5	7.8	271	14	US-10-224-880C-33	Sequence 33, Appl
22	74.5	7.8	332	14	US-10-182-960-13	Sequence 13, Appl
23	74.5	7.8	543	9	US-09-757-041-2	Sequence 2, Appl
24	74.5	7.8	543	14	US-10-004-378A-35	Sequence 35, Appl
25	74.5	7.8	939	14	US-10-369-493-3816	Sequence 3816, Ap
26	74	7.8	399	15	US-10-424-599-225192	Sequence 225192,
27	74	7.8	566	8	US-08-813-323A-1	Sequence 1, Appl
28	74	7.8	567	14	US-10-247-212-7	Sequence 7, Appl
29	74	7.8	567	14	US-10-207-655-103	Sequence 103, App
30	74	7.8	568	8	US-08-813-323A-2	Sequence 2, Appl
31	74	7.8	568	14	US-10-116-275-173	Sequence 173, App
32	74	7.8	568	14	US-10-004-378A-36	Sequence 36, Appl
33	74	7.8	568	15	US-10-042-865-166	Sequence 166, App
34	74	7.8	819	16	US-10-437-963-184313	Sequence 184313,
35	74	7.8	1326	16	US-10-437-963-129340	Sequence 129340,
36	73.5	7.7	345	15	US-10-335-977-6130	Sequence 6130, Ap
37	73.5	7.7	346	15	US-10-335-977-6131	Sequence 6131, Ap
38	73.5	7.7	609	14	US-10-372-686-6	Sequence 6, Appl
39	73.5	7.7	609	14	US-10-371-558-6	Sequence 6, Appl
40	73.5	7.7	609	14	US-10-375-553-6	Sequence 6, Appl
41	73.5	7.7	609	15	US-10-372-553-6	Sequence 6, Appl
42	73.5	7.7	1419	16	US-10-437-963-125464	Sequence 125464,
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44	73	7.7	313	15	US-10-424-599-221929	Sequence 221929,
45	73	7.7	389	9	US-09-767-041-17	Sequence 17, Appl

#### ALIGNMENTS

RESULT 1  
US-10-080-455-1  
; Sequence 1, Application US/10080455  
; Publication No. US20020146389A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Mark, Melanie R.  
; APPLICANT: Marsters, Scott A.  
; APPLICANT: Pictl, Robert M.  
; TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog  
; FILE REFERENCE: P150R2  
; CURRENT APPLICATION NUMBER: US/10/080,455  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/195,368  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: US 60/069,661  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: US 60/065,635  
; PRIOR FILING DATE: 1997-11-18  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 1  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-080-455-1

Query Match 100.0%; Score 951; DB 13; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENNPLSHSRTOGA...R...K...M...P...S...T...M...L...F...L...G...S...W...L...I...F...I...O...L...E...T...A...K...E...P...C...M...A 60  
DB 1 MCLSHLENNPLSHSRTOGA...R...S...W...K...I...M...L...F...C...S...I...V...M...L...F...L...C...S...W...L...I...F...I...O...L...E...T...A...K...E...P...C...M...A 60

QY 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANNVDVAPFEVRLYKN 120  
Db 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANNVDVAPFEVRLYKN 120  
QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177  
Db 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177

RESULT 2  
US-10-116-378-16  
; Sequence 16, Application US/10116378  
; Publication No. US2002015093A1

; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin  
; APPLICANT: Masters, Scott A.  
; APPLICANT: Pitti, Robert M.  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND  
; TITLE OF INVENTION: NUCLEIC  
; TITLE OF INVENTION: ACTIS ENCODING THE SAME  
; FILE REFERENCE: P1206R1  
; CURRENT APPLICATION NUMBER: US/10/116,378  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09  
; NUMBER OF SEQ ID NOS: 31  
; SEQ ID NO 16  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-116-378-16

Query Match 100.0%; Score 951; DB 13; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCISIVMLLFLCSPSWLIFFLQLETAKEPCMA 60  
QY 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANNVDVAPFEVRLYKN 120  
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QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177  
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RESULT 3  
US-10-151-882-39  
; Sequence 39, Application US/10151882  
; Publication No. US20030059862A1

; GENERAL INFORMATION:  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)  
; FILE REFERENCE: PF554  
; CURRENT APPLICATION NUMBER: US/10/151,882  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293,100  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 39  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-151-882-39

Query Match 100.0%; Score 951; DB 14; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCISIVMLLFLCSPSWLIFFLQLETAKEPCMA 60  
Db 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCISIVMLLFLCSPSWLIFFLQLETAKEPCMA 60  
QY 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANNVDVAPFEVRLYKN 120  
Db 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANNVDVAPFEVRLYKN 120  
QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177  
Db 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177

RESULT 4  
US-10-218-547-40  
; Sequence 40, Application US/10218547  
; Publication No. US20030100074A1

; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel  
; TITLE OF INVENTION: Human Endokine Alpha  
; FILE REFERENCE: PF561  
; CURRENT APPLICATION NUMBER: US/10/218,547  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/312,542  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/330,761  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: human  
US-10-218-547-40

Query Match 100.0%; Score 951; DB 14; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCISIVMLLFLCSPSWLIFFLQLETAKEPCMA 60  
Db 1 MCLSHLENMPLSHSRTOGAQRSSWKLMLFCISIVMLLFLCSPSWLIFFLQLETAKEPCMA 60  
QY 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANNVDVAPFEVRLYKN 120  
Db 61 KFGPLPSKQWASSSEPPCVNKVSDMKLEILLQNGLYLYIGQVAPNANNVDVAPFEVRLYKN 120  
QY 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177  
Db 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI.FNSEHQVLYKNNYWGIIILLANPQFIS 177

RESULT 5  
US-10-310-793-44  
; Sequence 44, Application US/10310793  
; Publication No. US20030198640A1

; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Zhang, Jun  
; APPLICANT: Wei, Bing  
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases  
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta  
; FILE REFERENCE: PF573  
; CURRENT APPLICATION NUMBER: US/10/310,793



;; CURRENT FILING DATE: 2002-12-06  
;; PRIOR APPLICATION NUMBER: 60/336,695  
;; PRIOR FILING DATE: 2001-12-07  
;; PRIOR APPLICATION NUMBER: 10/226,294  
;; PRIOR FILING DATE: 2002-08-23  
;; PRIOR APPLICATION NUMBER: 60/314,381  
;; PRIOR FILING DATE: 2001-08-24  
;; PRIOR APPLICATION NUMBER: 09/899,059  
;; PRIOR FILING DATE: 2001-07-06  
;; PRIOR APPLICATION NUMBER: 60/278,449  
;; PRIOR FILING DATE: 2001-03-26  
;; PRIOR APPLICATION NUMBER: 60/216,879  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 09/559,290  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 60/180,908  
;; PRIOR FILING DATE: 2000-02-08  
;; PRIOR APPLICATION NUMBER: 60/134,067  
;; PRIOR FILING DATE: 1999-05-13  
;; PRIOR APPLICATION NUMBER: 60/132,227  
;; PRIOR FILING DATE: 1999-05-03  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 71  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 44  
;; LENGTH: 177  
;; TYPE: PRT  
;; ORGANISM: human  
US-10-310-793-44

Query Match 100.0%; Score 951; DB 14; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MCISHENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSFWSWIFIFLOLETAKEPCMA 60  
DB 1 MCISHENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSFWSWIFIFLOLETAKEPCMA 60  
QY 61 KFGPLPSKQWMASSPEPCNVKSDWKLETLONGLYLYGOVAPNANNDVAPFEVRLYKN 120  
DB 61 KFGPLPSKQWMASSPEPCNVKSDWKLETLONGLYLYGOVAPNANNDVAPFEVRLYKN 120  
QY 121 KDMIQTLTKSKIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILLANPQFIS 177  
DB 121 KDMIQTLTKSKIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILLANPQFIS 177

RESULT 6  
US-10-202-062-40  
;; Sequence 40, Application US/10202062  
;; Publication No. US20040038349A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Human Genome Sciences, Inc.,  
;; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members  
;; FILE REFERENCE: PF559  
;; CURRENT APPLICATION NUMBER: US/10/202,062  
;; CURRENT FILING DATE: 2002-07-25  
;; PRIOR APPLICATION NUMBER: 60/307,838  
;; PRIOR FILING DATE: 2001-07-27  
;; NUMBER OF SEQ ID NOS: 42  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 40  
;; LENGTH: 177  
;; TYPE: PRT  
;; ORGANISM: human  
US-10-202-062-40

Query Match 100.0%; Score 951; DB 15; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MCISHENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSFWSWIFIFLOLETAKEPCMA 60  
DB 1 MCISHENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSFWSWIFIFLOLETAKEPCMA 60

DB 1 MCISHENMPLSHSRTOGAQRSSWKLMLFCSIVMLFLCSFWSWIFIFLOLETAKEPCMA 60  
QY 61 KFGPLPSKQWMASSPEPCNVKSDWKLETLONGLYLYGOVAPNANNDVAPFEVRLYKN 120  
DB 61 KFGPLPSKQWMASSPEPCNVKSDWKLETLONGLYLYGOVAPNANNDVAPFEVRLYKN 120  
QY 121 KDMIQTLTKSKIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILLANPQFIS 177  
DB 121 KDMIQTLTKSKIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILLANPQFIS 177

RESULT 7  
US-09-345-790-2  
;; Sequence 2, Application US/09345790  
;; Patent No. US20020099198A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Yu, Guo-Liang  
;; APPLICANT: Ni, Jian  
;; APPLICANT: Rosen, Craig A.  
;; TITLE OF INVENTION: Human Endokine Alpha  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
;; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
;; CITY: WASHINGTON  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/345,790  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/912,227  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Steffe, Eric K.  
;; REGISTRATION NUMBER: 36,688  
;; REFERENCE/DOCKET NUMBER: 1488.0470001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 169 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-345-790-2

Query Match 95.3%; Score 906; DB 9; Length 169;  
Best Local Similarity 100.0%; Pred. No. 1.1e-87;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 MFLSHSRTOGAQRSSWKLMLFCSIVMLFLCSFWSWIFIFLOLETAKEPCMAKFGPLPSK 68  
DB 1 MFLSHSRTOGAQRSSWKLMLFCSIVMLFLCSFWSWIFIFLOLETAKEPCMAKFGPLPSK 68  
QY 69 WQMASSPEPCNVKSDWKLETLONGLYLYGOVAPNANNDVAPFEVRLYKNKDMIQTLT 128  
DB 61 WQMASSPEPCNVKSDWKLETLONGLYLYGOVAPNANNDVAPFEVRLYKNKDMIQTLT 128  
QY 129 NKSQIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILLANPQFIS 177  
DB 121 NKSQIQNVGTYELHVGDTIDLFNSEHQVLRKNTYWGIIILLANPQFIS 169

RESULT 8

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US-10-136-511-2
; Sequence 2, Application US/10136511
; Publication No. US20020168729A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
; FILE REFERENCE: 1488.0470007/EKS/PSC
; CURRENT APPLICATION NUMBER: US/10/136,511
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/513,584
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/345,790
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/136,788
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/122,099
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 08/912,227
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: 60/024,058
; PRIOR FILING DATE: 1996-08-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-136-511-2
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Query Match 95.3%; Score 906; DB 13; Length 169;

Best Local Similarity 100.0%; Pred. No. 1.1e-87; Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 9 MPLSHRTOGAQRSSWKMLFCSYVMTLFLCSFWLFIPLQLEFAKPCMAKFGPLPSK 68
DB 1 MPLSHRTOGAQRSSWKMLFCSYVMTLFLCSFWLFIPLQLEFAKPCMAKFGPLPSK 60
QY 69 WOMASSEPPCVNKVSDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRLYKXKMIQTLT 128
DB 61 WOMASSEPPCVNKVSDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRLYKXKMIQTLT 120
QY 129 NKSKIQNVGTYELHVGDTIDLIENSHOVLKNTYWGIIILLANQFIS 177
DB 121 NKSKIQNVGTYELHVGDTIDLIENSHOVLKNTYWGIIILLANQFIS 169
```

RESULT 9

```
US-10-338-083-17
; Sequence 17, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahljat, Basil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-17
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Query Match 63.9%; Score 608; DB 14; Length 113;

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Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 58 CMAKFGPLPSKQWASSPPCVNKVSDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRL 117
DB 1 CMAKFGPLPSKQWASSPPCVNKVSDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRL 60
QY 118 YKXKDMIQTLTNKSKIQNVGTYELHVGDTIDLIENSHOVLKNTYWGIIILL 170
DB 61 YKXKDMIQTLTNKSKIQNVGTYELHVGDTIDLIENSHOVLKNTYWGIIILL 113
```

RESULT 10

```
US-10-611-399-17
; Sequence 17, Application US/10611399
; Publication No. US20040170602A1
; GENERAL INFORMATION:
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahljat, Basil I.
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
; FILE REFERENCE: A-71273-3
; CURRENT APPLICATION NUMBER: US/10/611,399
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-611-399-17
```

Query Match 63.9%; Score 608; DB 16; Length 113;

Best Local Similarity 100.0%; Pred. No. 2.4e-56; Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 58 CMAKFGPLPSKQWASSPPCVNKVSDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRL 117
DB 1 CMAKFGPLPSKQWASSPPCVNKVSDWKLEILQNGLYLIYGVAPNANYNDVAPFEVRL 60
QY 118 YKXKDMIQTLTNKSKIQNVGTYELHVGDTIDLIENSHOVLKNTYWGIIILL 170
DB 61 YKXKDMIQTLTNKSKIQNVGTYELHVGDTIDLIENSHOVLKNTYWGIIILL 113
```

RESULT 11

```
US-09-864-761-48455
; Sequence 48455, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
```

```

; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48455
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031599.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EST HUMAN HIT: BB270854.1, EVALU6 6.50e-01
; OTHER INFORMATION: SWISSPROT HIT: P25003, EVALU6 1.20e+00
US-09-864-761-48455
```

```

Query Match          29.5%; Score 281; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.7e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

Qy      1 MCLSHENMPLSHSRTOGAORSSWKLMLFCSTIVMLFLCFSFSLFIPIQLE 52
Db      1 MCLSHENMPLSHSRTOGAORSSWKLMLFCSTIVMLFLCFSFSLFIPIQLE 52
```

```

RESULT 12
US-10-295-027-280
; Sequence 280, Application US/10295027
; Publication No. US2003023250A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natacha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glyme, Richard
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
```

```

; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 280
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-280
```

```

Query Match          9.0%; Score 85.5; DB 14; Length 377;
Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 32; Conservative 31; Mismatches 54; Indels 37; Gaps 6;
```

```

Qy      26 LMLFCSIYV--LLFCFSFSLFIPIQLETAKEPCGAKGPIPSKQWASSPPCYNKKS 83
Db      127 IMFCKIVNPSAININPVLITLLLELIMATVITA-----ARSSBDCKK-- 174
Qy      84 DWKLEILONGLYLIGQVAPNANYNDVAPFEVRLYKNMDIOTLTKSKIQWVGTYELH 143
Db      175 -----KGSMSDSANIDDEVFPARVLKSVSEVVIAGISAV--LGGITALN 218
Qy      144 VGDITDILFNSHQVLXNNTYTGITLLANPOTIS 177
Db      219 VDDSV-----SGPHLSV--TFFWITLVACFSAIA 245
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```

RESULT 13
US-10-424-599-201262
; Sequence 201262, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201262
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(246)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23765C.1.pcp
US-10-424-599-201262
```

```

Query Match          8.4%; Score 79.5; DB 15; Length 246;
Best Local Similarity 22.9%; Pred. No. 6.1;
Matches 36; Conservative 21; Mismatches 55; Indels 45; Gaps 6;
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[illegible]

```

RESULT 14
US-10-149-310-52
Sequence 52, Application US/10149310
Publication No. US20040077039A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
APPLICANT: Maxon, Mary
APPLICANT: Sherman, Amir
TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
TITLE OF INVENTION: Zinc Binuclear Cluster Proteins
FILE REFERENCE: 14184-019US1
CURRENT APPLICATION NUMBER: US/10/149,310
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/US01/29288
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: US 60/233,564
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52
LENGTH: 879
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-149-310-52

```

```

Query March 31, 2001
Best Local Similarity 22.7%; Pred. No. 32;
Matches 37; Conservative 36; Mismatches 53; Indels 37; Gaps 8

8.4%; Score 79.5; DB 15; Length 879;

      45 IFIFLQ---ETAKPECNAA-----FGPLPSKQWASSEPPCCVKY----- 82
      554 IFFFLKLTQDSALDQVAKETIVLPSEEDDYKKLDTLSNATSSSEPRVDVQGLFRE 613
      83 ----SDWK--LEIILONGLYLIVGQVAPNAN-----NDVAPFEVRLYKNQDMTQTLNRSK 132
      614 ALNNDGKHHIEFVEKPIINVSADSTPSSITPIPTNTA---TESYKNSKDSISLVSKTD 670
      133 IONVGATYELH-VGDTIDLIENSEHOVLKNNTYWGIIILANDQ 174
      671 -ENIGTDSLVLGFLPMSLLILFSDCVRIYVHNEXNYMLTYLPIVER 712

RESULT 15
US-10-149-310-50
; Sequence 50, Application US/10149310
; Publication No. US2004007039A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; APPLICANT: Madden, Kevin T.
; APPLICANT: Maxon, Mary
; APPLICANT: Sherman, Amir
; TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
; TITLE OF INVENTION: Zinc Binuclear Cluster Proteins
; FILE REFERENCE: 14184-019US1
; CURRENT APPLICATION NUMBER: US/10/149,310
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US01/29288
; PRIOR FILING DATE: 2001-09-19

```

```

1      PRIOR APPLICATION NUMBER: 09/6233,564
2      PRIOR FILING DATE: 2000-09-19
3      NUMBER OF SEQ. ID NOS: 308
4      SOFTWARE: PatentIn version 3.1
5      SEQ. ID NO. 50
6      LENGTH: 880
7      TYPE: RAT
8      ORGANISM: Saccharomyces cerevisiae
9      US-10-149-310-50

```

	Query Match	8.1%	Score 77.5	DB 15	Length 880
	Best Local Similarity	22.7%	Pred. No. 52		
	Matches	37	Conservative	35	Mismatches 54
					Indels 37
					Gaps 8
QY	45	IFIFQL--ETAKEPCMAK-----	FGPIPSKQMASSPPPCNKY-----	82	
DB	555	IFSFKLQDSTALDKRAKEVILPSEEDDNYKPLDTSNATTSSESPRDVVOEGIFRE	614		
QY	83	----SDMK--LEIDONGLYLYIGQVAPNAN--	NVDVAPFEVRLTKXNDMIQTLTNKSK	132	
DB	615	ALNNDGKIHIEFVEPELTNVSADSTPSSITPPPIFNIA--	TESYNNKSDISKLVSKTD	671	
QY	133	IQNVGQTEYELH--VGDTIDILFNSEQVLENNNTYTGIIILLANPO	174		
DB	672	-ENIGTDSLYGLPNSLILLFSDCVRIVAHNEVNNLTYPVPR	723		

Search completed: November 2, 2004, 12:52:46  
Job time : 130 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2004, 12:27:21 / Search time 39 Seconds  
(without alignments)  
300.982 Million cell updates/sec

Title: US-10-080-455-1

Perfect score: 951

Sequence: 1 MCISHLENNPLSHSRTOGAQ.....VLKNTYWGILLANPQFIS 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	906	95.3	169	2	US-08-912-227-2
2	906	95.3	169	4	US-09-513-584-2
3	906	95.3	169	4	US-09-345-790-2
4	84.5	8.9	1221	4	US-09-107-532A-3959
5	77.5	8.1	880	4	US-09-538-092-601
6	77	8.1	217	4	US-09-248-796A-20671
7	77	8.1	326	3	US-08-089-397A-11
8	77	8.1	326	6	5395759-2
9	77	8.1	2763	3	US-08-496-944-2
10	75.5	7.9	550	3	US-09-039-859-9
11	75	7.9	325	4	US-09-328-352-5760
12	74.5	7.8	271	4	US-09-443-041A-33
13	74.5	7.8	543	3	US-08-697-610-2
14	74.5	7.8	543	3	US-08-349-357-2
15	74	7.8	157	5	PCT-US93-02475-6
16	74	7.8	235	4	US-09-270-767-49088
17	74	7.8	567	4	US-09-645-926A-7
18	73.5	7.7	609	4	US-09-396-149-6
19	73	7.7	166	3	US-08-765-381-12
20	73	7.7	289	4	US-09-248-796A-15058
21	72.5	7.6	721	4	US-09-248-796A-18800
22	72	7.6	545	4	US-09-538-092-59
23	71.5	7.5	233	1	US-08-323-445A-10
24	71.5	7.5	233	1	US-08-515-903A-10
25	71.5	7.5	233	2	US-08-912-227-3
26	71.5	7.5	233	2	US-08-230-428B-2
27	71.5	7.5	233	3	US-08-883-086-6

28	71.5	7.5	233	3	US-08-880-342-37	Sequence 37, Appl
29	71.5	7.5	233	4	US-09-589-287B-3	Sequence 3, Appl
30	71.5	7.5	233	4	US-09-513-584-3	Sequence 3, Appl
31	71.5	7.5	233	4	US-09-157-864-9	Sequence 9, Appl
32	71.5	7.5	233	4	US-10-082-260-5	Sequence 5, Appl
33	71.5	7.5	233	4	US-09-345-790-3	Sequence 3, Appl
34	71.5	7.5	233	4	US-09-982-308B-22	Sequence 22, Appl
35	71.5	7.5	233	4	US-09-879-919-5	Sequence 5, Appl
36	71.5	7.5	233	4	US-09-588-947A-3	Sequence 3, Appl
37	71.5	7.5	233	4	US-09-131-237C-3	Sequence 3, Appl
38	71.5	7.5	233	4	US-09-589-286A-3	Sequence 3, Appl
39	71.5	7.5	233	4	US-09-005-874-3	Sequence 3, Appl
40	71.5	7.5	233	4	US-09-255-794A-3	Sequence 3, Appl
41	71.5	7.5	233	5	PCT-US93-12840-10	Sequence 10, Appl
42	71.5	7.5	233	6	5422425-2	Patent No. 5422425
43	71.5	7.5	633	3	US-08-860-048-11	Sequence 11, Appl
44	71.5	7.5	633	4	US-09-838-586-11	Sequence 11, Appl
45	71	7.5	157	5	PCT-US93-02475-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-912-227-2  
; Sequence 2, Application US/08912227  
; Patent No. 5998171  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Human Endokine Alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,227  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,058  
; FILING DATE: 16-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0470001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-912-227-2

Query Match 95.3%; Score 906; DB 2; Length 169;

Best Local Similarity 100.0%; Pred. No. 2.8e-99;

Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MPISHSRTOGAOSSWKLWFCISVWMLPCLCSWILFIFLOLETAKEPCMAKRGPIPSK 68

Db 1 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFIQLETAKPCPAKFGPLPSK 60  
QY 69 WQMASSEPPCVNKKVSDWMLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 128  
Db 61 WQMASSEPPCVNKKVSDWMLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 120  
QY 129 NKSXIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 177  
Db 121 NKSXIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 169

## RESULT 2

US-09-513-584-2  
; Sequence 2, Application US/09513584  
; Patent No. 6406867  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Human Endokine Alpha and Methods  
; TITLE OF INVENTION: of Use  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX,  
; ADDRESS: P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/513,584  
; FILING DATE: 25-FEB-2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,058  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,227  
; FILING DATE: 15-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/122,099  
; FILING DATE: 26-FEB-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/136,788  
; FILING DATE: 28-MAY-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/345,790  
; FILING DATE: 01-JUL-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0470005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-513-584-2

Query Match 95.3%; Score 906; DB 4; Length 169;  
Best Local Similarity 100.0%; Pred. No. 2.8e-99;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFIQLETAKPCPAKFGPLPSK 68  
Db 1 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFIQLETAKPCPAKFGPLPSK 60  
QY 69 WQMASSEPPCVNKKVSDWMLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 128  
Db 61 WQMASSEPPCVNKKVSDWMLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 120  
QY 129 NKSXIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 177  
Db 121 NKSXIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 169

## RESULT 3

US-09-345-790-2  
; Sequence 2, Application US/09345790  
; Patent No. 6521742  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Human Endokine Alpha  
; TITLE OF INVENTION: of Use  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/345,790  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/912,227  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0470001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-345-790-2

Query Match 95.3%; Score 906; DB 4; Length 169;  
Best Local Similarity 100.0%; Pred. No. 2.8e-99;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFIQLETAKPCPAKFGPLPSK 68  
Db 1 MFLSHRTQGAQRSSWKMLFCSIVMLFLCSFSLIFIFIQLETAKPCPAKFGPLPSK 60  
QY 69 WQMASSEPPCVNKKVSDWMLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 128  
Db 61 WQMASSEPPCVNKKVSDWMLLEILQNGLYLIYGQVAPNANYNDVAPPEVLYNKKMIQTLT 120  
QY 129 NKSXIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 177  
Db 121 NKSXIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPOFIS 169

```
RESULT 4
US-09-107-532A-3959
; Sequence 3959, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3959:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1221 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1221
; SEQUENCE DESCRIPTION: SEQ ID NO: 3959:
US-09-107-532A-3959

Query Match      8.9%; Score 84.5; DB 4; Length 1221;
Best Local Similarity 28.8%; Pred. No. 1.4;
Matches 19; Conservative 19; Mismatches 23; Indels 5; Gaps 1;

QY 102 APNANNDVAFEFVRLYKNDMIOQLTNKS-----KQNVGTYELHVDITDILFNSEH 156
DB 515 APNGYQIDSESEFSTIVAKNONVTTTRTKKSTGSEVEIKTIGLDGLPLNVEFTIYSDN 574
QY 157 QVLKNN 162
DB 575 KVVKDN 580

RESULT 5
US-09-538-092-601
; Sequence 601, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
```

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; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: Curataseqformatter Version 0.9
; SEQ ID NO 601
; LENGTH: 880
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YML099C
US-09-538-092-601

Query Match      8.1%; Score 77.5; DB 4; Length 880;
Best Local Similarity 22.7%; Pred. No. 6;
Matches 37; Conservative 35; Mismatches 54; Indels 37; Gaps 8;

QY 45 IFIFIQI---ETAKEPCMAK-----FGPLPSKQWASSSEPCVKNKY----- 82
DB 555 IFSFKLIDSTALDKVRAKEIYILPSEEDNKKPLDTSNATSSSEPRVDVVOEGLFRE 614
QY 83 ----SPWK--LELQNGKXIIYGOVAPNAN----YNDVAFEFVRLYKNDMIOQLTNKSK 132
DB 615 ALNENDGKHIEFEKPIITVNSDSTPSSTPEIFTNIA---TESYNNKSDISKLVSKTD 671
QY 133 IQNVGTYELH-VGDTIDILFNSEHQLKNNYWGIIILANPQ 174
DB 672 -ENITGDSLYGLPNSIILFSDCKRIVRNNEYNYLTLPVPR 713

RESULT 6
US-09-248-796A-20671
; Sequence 20671, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196,132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20671
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (15)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknc
US-09-248-796A-20671

Query Match      8.1%; Score 77; DB 4; Length 217;
Best Local Similarity 27.2%; Pred. No. 0.84;
Matches 31; Conservative 13; Mismatches 44; Indels 26; Gaps 7;

QY 66 PSKQWASS--EPP-----CVNKVSDWKLEILQNGLYLTYGOVAP-----NANYNDVAPF 113
DB 85 PKQWMDAEKQWEPPLVNPFCATGCGWEAPLIPNDHYI--GWPFPDINKPNVNGI--W 140
QY 114 EVRLYKNDMIOQLTNKSKIQNVGT-YELHVDITDILFNSEHQLKNNYWG 166
DB 141 TPRLINPDIYYQVKTGKLDKPIGIGIFEL-----WSISDILFDNIYIG 185
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RESULT 7
US-08-089-397A-11
; Sequence 11, Application US/08089397A
; Patent No. 6086880
; GENERAL INFORMATION:
; APPLICANT: SABARA, MARTA I.J.
; APPLICANT: FRENCHICK, PATRICK J.
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: IJAZ, MOHAMMAD K.
; APPLICANT: GILCHRIST, JAMES E.
; APPLICANT: REDMOND, MARK J.
; TITLE OF INVENTION: ROTAVIRUS VACCINES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/089,397A
; FILING DATE: 07-JUL-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 29311-20003.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-089-397A-11

Query Match      8.1%; Score 77; DB 3; Length 326;
Best Local Similarity 22.8%; Pred. No. 1.6;
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY 26 LMLFCSIYMLFLC-----SFSWLIFFILOETAKPCMAK-----FGPLPSKQW 71
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 LTLISILNLNYLKTITNTMDYILFRFLILALISPVRTQNYGMVLPITGSLDAVYTN 69
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 ASSEPP-----CV-----NKVSDWKLEILONGGLYLYGVAPNA--NYNDVAPPEV 115
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 70 STSGEPFLSTLCYYPAKAKNEISDDDEMENTLSQLFLTKGPIGSVYFKYNDINTISV 129
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 --RLYKKNKDMIQTLTKNSKIQNVGQTYELHVGDTIDLIENSEHQVLKNNYTGIIILANP 173
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 130 NPQLYCDYNVV-----LMRYDNTSELDASELADLILNE-----W-----LCNP 167
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 QFIS 177
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 168 MDIS 171
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
5395759-2
; Patent No. 5395759
; APPLICANT: HOLMES, IAN H.; DYALL-SMITH, MICHAEL L.
; TITLE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCE
```

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; ENCODING THE HUMAN ROTAVIRUS MAJOR OUTER CAPSID GLYCOPROTEIN
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/474,642
; FILING DATE: 29-APR-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 824,704
; FILING DATE: 04-FEB-1987
; SEQ ID NO:2:
; LENGTH: 326
; 5395759-2

Query Match      8.1%; Score 77; DB 6; Length 326;
Best Local Similarity 22.8%; Pred. No. 1.6;
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY 26 LMLFCSIYMLFLC-----SFSWLIFFILOETAKPCMAK-----FGPLPSKQW 71
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 LTLISILNLNYLKTITNTMDYILFRFLILALISPVRTQNYGMVLPITGSLDAVYTN 69
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 ASSEPP-----CV-----NKVSDWKLEILONGGLYLYGVAPNA--NYNDVAPPEV 115
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 70 STSGEPFLSTLCYYPAKAKNEISDDDEMENTLSQLFLTKGPIGSVYFKYNDINTISV 129
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 --RLYKKNKDMIQTLTKNSKIQNVGQTYELHVGDTIDLIENSEHQVLKNNYTGIIILANP 173
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 130 NPQLYCDYNVV-----LMRYDNTSELDASELADLILNE-----W-----LCNP 167
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 QFIS 177
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 168 MDIS 171
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-08-496-944-2
; Sequence 2, Application US/08496944
; Patent No. 6040496
; GENERAL INFORMATION:
; APPLICANT: Law, Marcus D
; APPLICANT: Dietz, Jon M
; TITLE OF INVENTION: Use of Translationally altered RNA to
; TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,944
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1814
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-496-944-2

Query Match      8.1%; Score 77; DB 3; Length 2763;
```



Best Local Similarity 25.0%; Pred. No. 38;  
Matches 31; Conservative 20; Mismatches 53; Indels 20; Gaps 5;

QY 51 LERAKPCWAKFGPLSKQMASSEPPCVNKKSDMKLEILQNGLYLYGVANANYNV 110  
18 IOPFKRCNDKFSHLPLMQVAETLGHYTNOCKQMDV-SEALIKNTLTPDDAKKASA 76  
DB 111 APEV-RLYKNC-----DMIQTLTNKSKIQNGVTELVHVDITDILFENSEHQVLN-N 162  
77 ALLEVERWYKNRKESLKTDSLESFRK-----ISPKSTINAMLCNDQJLKNAN 125

QY 163 TYWG 166  
126 FVWG 129

DB 126 FVWG 129

RESULT 10  
US-09-039-859-9  
; Sequence 9, Application US/09039859  
; Patent No. 6063987  
; GENERAL INFORMATION:  
; APPLICANT: Daub, Margaret E.  
; APPLICANT: Ehrenshaft, Marilyn  
; APPLICANT: Jenns, Ann E.  
; TITLE OF INVENTION: Isolated Genes and Proteins Encoding  
; TITLE OF INVENTION: Resistance to Photosensitizers  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Virginia C. Bennett  
; STREET: PO Box 37428  
; CITY: Raleigh  
; STATE: No. 6063987ch Carolina  
; COUNTRY: US  
; ZIP: 27627  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,859  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bennett, Virginia C.  
; REGISTRATION NUMBER: 37,092  
; REFERENCE/DOCKET NUMBER: 5405.333  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-854-1400  
; TELEFAX: 919-854-1401  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 550 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-039-859-9

Query Match 7.9%; Score 75.5; DB 3; Length 550;  
Best Local Similarity 18.5%; Pred. No. 5.1;  
Matches 43; Conservative 33; Mismatches 55; Indels 101; Gaps 13;

QY 12 SHSRTOGAQRSSWKLWFC---SIVMLFLF---CSFSLMFLFIQLETAKEPCWAKGPL 65  
188 SYSSVEG-----WRAWLGCHVLSVMAIFRKSMNTASWT---EQHEQAR-LMLQYSPL 236  
QY 66 ---PSRK-----QMASSBP-PCVNKVSQWKLKI- 89  
DB 237 NADSDRWLAQYIRAERLCEEVSEQVDLTNTSFYRDVADPATRNPVQCGRKIKLNMWKGVP 296  
QY 90 --LQNGLYLYGVANANYNVAFPEVRLYKNCMDIQLTNKSK----- 133  
DB 297 QRLRSPLIMWEHVA-----TAYMHEPVLHTATNKNDSFTAPYLAERLSITDF 343

QY 134 -----QNVGTYEL--HVGDITDILFENSEHQVLKNNTYWGIIILANPOFI 176  
DB 344 PRLVYQDHITAVYELHTAIVQAVLDLFINVDK-----SLVASSISLV 385

RESULT 11  
US-09-328-352-5760  
; Sequence 5760, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5760  
; LENGTH: 325  
; TYPE: PRN  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5760

Query Match 7.9%; Score 75; DB 4; Length 325;  
Best Local Similarity 25.8%; Pred. No. 2.7;  
Matches 42; Conservative 25; Mismatches 56; Indels 40; Gaps 8;

QY 31 SYVMLFLCSFSLMFLFIQLETAKEPCWAKFGPLSKQMASSEPPCVNKKV-----SDW 85  
DB 80 SYVFLFGISLMPVTVYIINI-----VNKY--LPSHEKIRDDLPFPKISITFTASIW 130  
QY 86 KLEIILQNGLYLYGYVA--PNANYNDVAPPEVRLYKNCMDIQLTNKSKIQNGVTELVH 143  
DB 131 FIYILRN-LHLYWQVSLYVGCTVSWIAFLYAFYVNOQDIKFSKKFK-----N 179

QY 144 VGDITDILFNSEH-----QVLKNNTYWGIIILANP 173  
DB 180 IEDIIDIGASEHLKIFARDKJLKELETNKNLSIHVAIFLIVTP 222

RESULT 12  
US-09-443-041A-33  
; Sequence 33, Application US/09443041A  
; Patent No. 6465717  
; GENERAL INFORMATION:  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Orozco, Buddy  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Shen, Jennie  
; TITLE OF INVENTION: Sterol Metabolism Enzymes  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/443,041A  
; CURRENT FILING DATE: 1999-11-18  
; PRIOR APPLICATION NUMBER: 60/109,283  
; PRIOR FILING DATE: 1998-11-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 33  
; LENGTH: 271  
; TYPE: PRN  
; ORGANISM: Nicotiana tabacum  
US-09-443-041A-33

Query Match 7.8%; Score 74.5; DB 4; Length 271;  
Best Local Similarity 22.7%; Pred. No. 2.3;  
Matches 34; Conservative 23; Mismatches 50; Indels 43; Gaps 9;

QY 10 PLSHSRTOGAQRSSWKLWFC---FCSIYMLFLFCSFSLMFLFI----- 48  
DB 31 PLPH-MLQG-----WLRNRYIGVULYISGFLWCFYIYHKKRVVYIPKDAIPSKAM 81  
QY 49 -IQLETAKEPCWAKFGPLP--SKWQMASSBPCCVNKVSQD--WLEIILQNGLYLI---YQG 100

DB 82 LLQISVANK-AMPTWCALPSEVMIENGMTCEFRISDVGLSVIYAALIVVERGI 140  
QY 101 VAPNANVDAPEVRLYKXKMDIQTITNK 130  
DB 141 YMHMEHLDIKP---LYKYIATHHTYK 166

## RESULT 13

US-08-697-610-2  
; Sequence 2, Application US/08697610  
; Patent No. 6172187  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Sato, Takaaki  
; TITLE OF INVENTION: CD40 Associated Proteins  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/697,610  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/349,357  
; FILING DATE: 02-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 1203  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 543 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-697-610-2

Query Match 7.8%; Score 74.5; DB 3; Length 543;

Best Local Similarity 25.5%; Pred. No. 6.6; Matches 36; Conservative 20; Mismatches 42; Indels 43; Gaps 8;

QY 30 CSIVMLFLCSEFSWLIFFLOLETAKEPCNAKFGPLPSKQWQMASSEPCVKNKVSIDW----- 85  
DB 199 CAVVSCPHKCSVQTL---LHSEGNOQIKX-----HEASAVQHVVLLKEMSNLSL 245  
QY 86 --KLEILLONGLYLYGGVAPNAN---YNDVAPPEVRLYKXKMDIQTITNKSQIONVGST 139  
DB 246 EKVSVLLQN-----ESVEKKKSIQSLHNQICSEFIEIERQKEMLR--NNESKI----- 291  
QY 140 YELHVGDTIDLIFNSEHQVLK 160  
DB 292 --LHLQRYID---SQAEKLR 306

## RESULT 14

US-08-349-357-2  
; Sequence 2, Application US/08349357  
; Patent No. 6265556  
; GENERAL INFORMATION:

APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaaki  
TITLE OF INVENTION: CD40 Associated Proteins  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/349,357  
FILING DATE: 02-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 543 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-349-357-2

Query Match 7.8%; Score 74.5; DB 3; Length 543;

Best Local Similarity 25.5%; Pred. No. 6.6; Matches 36; Conservative 20; Mismatches 42; Indels 43; Gaps 8;

QY 30 CSIVMLFLCSEFSWLIFFLOLETAKEPCNAKFGPLPSKQWQMASSEPCVKNKVSIDW----- 85  
DB 199 CAVVSCPHKCSVQTL---LHSEGNOQIKX-----HEASAVQHVVLLKEMSNLSL 245  
QY 86 --KLEILLONGLYLYGGVAPNAN---YNDVAPPEVRLYKXKMDIQTITNKSQIONVGST 139  
DB 246 EKVSVLLQN-----ESVEKKKSIQSLHNQICSEFIEIERQKEMLR--NNESKI----- 291  
QY 140 YELHVGDTIDLIFNSEHQVLK 160  
DB 292 --LHLQRYID---SQAEKLR 306

## RESULT 15

PCT-US93-02475-6  
; Sequence 6, Application PC/TUS9302475  
; GENERAL INFORMATION:  
; APPLICANT: Winkleski, Bernadine J.  
; TITLE OF INVENTION: Tumor Necrosis Factor with Modified  
; TITLE OF INVENTION: Ion Channel  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Donald G. Lewis  
; STREET: 8328 Regents Road #1B  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage  
; COMPUTER: VE System 386  
; OPERATING SYSTEM: MS-DOS 5  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/02475  
FILING DATE: 19930412  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/852,625  
FILING DATE: 12 March 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Donald G. Lewis  
REGISTRATION NUMBER: 28636  
REFERENCE/DOCKET NUMBER: BJW-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2421  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: AMINO ACIDS  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Tumor Necrosis Factor (feline)  
PUBLICATION INFORMATION:  
AUTHORS: McGraw, R. A., Coffee, B.W., Otto,  
AUTHORS: C.M., Drews, R.T. and Rawling, C.A.  
TITLE: Gene Sequence of Feline Tumor Necrosis  
TITLE: Factor '  
JOURNAL: Nucleic Acids Research  
VOLUME: 18  
PAGES: 5564  
DATE: 1990  
RELEVANT RESIDUES IN SEQ ID NO: 6: 1-157  
PCT-US93-02475-6

Query Match 7.8%; Score 74; DB 5; Length 157;  
Best Local Similarity 24.4%; Pred. No. 1.2;  
Matches 30; Conservative 21; Mismatches 32; Indels 40; Gaps 6;

QY 81 KVSQDWKLEILQNGGLYLYIGGV-----APNANY---NDVAPFEVRLYKKNKMIQTLTNKS 131  
DB 42 ELTDNQKLPSPDSGLYLSQVLTGQGCSPSTHVLTHAIRFAVSYOTKYNLSAI--KS 99  
QY 132 KION-----VGGTYELHVGDTID-----LIFNSEHQVLKKNITYWGI 167  
DB 100 PCQRETPESGAERKWPWPPIYLGVPQLEKGRISTEINLPAYLDPAESGQV-----YFGI 154  
QY 168 ILL 170  
DB 155 IAL 157

Search completed: November 2, 2004, 12:42:27  
Job time : 41 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2004, 11:53:00 ; Search time 193 Seconds  
(without alignments)  
527.675 Million cell updates/sec

Title: US-10-080-455-1  
Perfect score: 951  
Sequence: 1 MCLSHLENNPLSHSRTOGAQ.....VLKNTYWGIIILANPQFIS 177

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	100.0	177	1	TN18 HUMAN
2	951	100.0	177	2	AAB69111
3	951	100.0	177	2	AAB69319
4	418.5	44.0	173	2	Q80YG2
5	418.5	44.0	173	2	CAE12166
6	418.5	44.0	173	2	CAE12167
7	414.5	43.6	173	2	Q7TMY2
8	412.5	43.4	173	2	Q7TSS5
9	412.5	43.4	173	2	AA055265
10	108.5	11.4	272	1	TNPS CHICK
11	88.5	9.3	273	2	Q74LW5
12	88.5	9.3	273	2	AA080050
13	86.5	9.1	516	2	Q861B8
14	85.5	9.0	270	2	Q896D6
15	85.5	9.0	376	1	MLC1 HUMAN
16	85.5	9.0	377	2	Q6NSI6
17	85.5	9.0	377	2	AAH70042
18	85.5	9.0	377	2	CAG30346
19	85	8.9	3063	2	Q8OXN1
20	84	8.8	579	2	Q6C5T4
21	84	8.8	2074	2	Q6C5T4
22	83.5	8.8	466	2	Q81A57
23	83	8.7	559	2	Q81A5
24	82	8.6	537	2	Q8GNC3
25	80.5	8.5	459	2	Q6HMY4
26	80	8.4	1181	2	Q96143
27	79.5	8.4	156	2	Q6D9W7
28	79.5	8.4	390	2	Q6LSR8
29	79.5	8.4	665	2	Q17701
30	79.5	8.4	847	2	Q6B1Y1
31	79.5	8.4	851	2	Q9LFL1

32	79	8.3	193	2	Q72VG7	Q72VG7 leptospira
33	79	8.3	193	2	Q8F914	Q8F914 leptospira
34	79	8.3	193	2	AA68957	AA68957 leptospira
35	79	8.3	326	2	Q805N8	Q805N8 human rotav
36	79	8.3	326	2	Q80AT3	Q80AT3 human rotav
37	79	8.3	372	1	PROB_OCEIH	Q8CUC5 oceanobacil
38	78.5	8.3	599	2	Q8E0H3	Q8E0H3 streptococc
39	78.5	8.3	599	2	Q8E648	Q8E648 streptococc
40	78.5	8.3	1061	2	Q7R934	Q7R934 plasmodium
41	78.5	8.3	1488	2	Q81DP7	Q81DP7 plasmodium
42	78	8.2	326	2	P89064	P89064 rotavirus
43	78	8.2	447	2	Q8GCK6	Q8GCK6 mycoplasma
44	78	8.2	564	1	Y61A MYCPN	P75041 mycoplasma
45	78	8.2	695	2	Q7R121	Q7R121 plasmodium

## ALIGNMENTS

RESULT 1  
TN18 HUMAN STANDARD; PRT; 177 AA.

AC Q9UNG2; Q95852; 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 18 (Glucocorticoid-induced TNF-related ligand) (hgtrll) (Activation-inducible TNF-related ligand) (AIRL) (UNQ149/PRO175).  
GN Name=TNFSF18; Synonyms=AIRL, GTRL, TL6;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Umbilical vein;  
RX MEDLINE=99175482; PubMed=10074428;  
RA Gurney A.L., Masters S.A., Huang A., Pitti R.M., Mark M., Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;  
RT "Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GTR.";  
RT Curr. Biol. 9:215-218(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Batton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S., Hang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshgiri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A., Vanden R., Watanabe C., Wleand D., Woods K., Xie W.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";  
RT Genome Res. 13:2265-2270(2003).  
RN [3]  
RP SEQUENCE OF 9-177 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=99156876; PubMed=10037686;  
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Yang I.-K., Kim Y.-J., Xing L., Liu D., Wang S.-X., Kwon B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand.";  
RT J. Biol. Chem. 274:6056-6061(1999).  
CC -!- FUNCTION: Cytokine that binds to TNFSF18/AIRR/GTR. Important for interactions between activated T lymphocytes and endothelial cells and may modulate T lymphocyte survival in peripheral tissues.  
CC -!- SUBUNIT: Homotrimer (Potential).

```

CC - SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC - TISSUE SPECIFICITY: Expressed at high levels in the small
CC intestine, ovary, testis, kidney and endothelial cells.
CC - INDUCTION: Up-regulated after stimulation by lipopolysaccharides.
CC - SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF125303; AAD22634.1; -
DR EMBL; AY358868; AAG99227.1; -
DR EMBL; AF117713; AAD19695.1; -
DR Genew; HGNC:11932; TNFSF18.
DR MIM; 603898; -
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; FALSE_NEG.
DR CycloLine; Glycoprotein; Signal-anchor; Transmembrane.
DR CycloLine; Glycoprotein; Signal-anchor (Potential).
DR TRANSMEM 1 28 Cytoplasmic (Potential).
DR TRANSMEM 29 49 Signal-anchor for type II membrane
DR TRANSMEM 50 177 Extracellular (Potential).
DR TRANSMEM 129 129 N-linked (GlcNAc...) (Potential).
DR TRANSMEM 161 161 N-linked (GlcNAc...) (Potential).
DR TRANSMEM 177 AA; 20307 MW; 3D78CEB90F4C9E3 CRC64;
SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB90F4C9E3 CRC64;

Query Match 100.0%; Score 951; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.2e-80;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPISHSRTOGAQRSSWKLWFCSTVWLFLFCSPFWLFIPLQETAKPMA 60
DB 1 MCLSHLEMPISHSRTOGAQRSSWKLWFCSTVWLFLFCSPFWLFIPLQETAKPMA 60
QY 61 KFGPLPSKQWASSEPPCVNKNVSDMKLEILONGYLITYGOVAPNANVNDVAPFEVRLTKN 120
DB 61 KFGPLPSKQWASSEPPCVNKNVSDMKLEILONGYLITYGOVAPNANVNDVAPFEVRLTKN 120
QY 121 KDMITLTNKSCKIQWVGTYELAHVGDITDILFNSEHGYLKNNTYWGIIILANPOFIS 177
DB 121 KDMITLTNKSCKIQWVGTYELAHVGDITDILFNSEHGYLKNNTYWGIIILANPOFIS 177

RESULT 2
AAH69111 PRELIMINARY; PRT; 177 AA.
ID AAH69111;
AC AAH69111;
DT 24-MAY-2004 (TREMBlrel. 27, Created)
DT 24-MAY-2004 (TREMBlrel. 27, Last sequence update)
DT 24-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE TNFSF18 protein (Fragment).
GN TNFSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Synthetic constructs;
RA MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Synthetic constructs;
RA Strausberg R.,
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069111; AAH69111.1; -
FT NON TER 1 1
SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB90F4C9E3 CRC64;

Query Match 100.0%; Score 951; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.2e-80;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPISHSRTOGAQRSSWKLWFCSTVWLFLFCSPFWLFIPLQETAKPMA 60
DB 1 MCLSHLEMPISHSRTOGAQRSSWKLWFCSTVWLFLFCSPFWLFIPLQETAKPMA 60
QY 61 KFGPLPSKQWASSEPPCVNKNVSDMKLEILONGYLITYGOVAPNANVNDVAPFEVRLTKN 120
DB 61 KFGPLPSKQWASSEPPCVNKNVSDMKLEILONGYLITYGOVAPNANVNDVAPFEVRLTKN 120
QY 121 KDMITLTNKSCKIQWVGTYELAHVGDITDILFNSEHGYLKNNTYWGIIILANPOFIS 177
DB 121 KDMITLTNKSCKIQWVGTYELAHVGDITDILFNSEHGYLKNNTYWGIIILANPOFIS 177

RESULT 3
AAH69319 PRELIMINARY; PRT; 177 AA.
ID AAH69319;
AC AAH69319;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE TNFSF18 protein.
GN TNFSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyanski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RA Strausberg R.;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC069319; AA069319.1; -  
 SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB90F4C9E3 CRC64;

Query Match 100.0%; Score 951; DB 2; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-80;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLEMPLSHRTGAGRSSWKMLFCSTVWLFICSPSWLIFFLQLETKAPECPMA 60  
 DB 1 MCLSHLEMPLSHRTGAGRSSWKMLFCSTVWLFICSPSWLIFFLQLETKAPECPMA 60  
 QY 61 KFGPLPSKQWQMASSEPPCVNKKVSDPKLEILLQNGLYLYIGQVAPNANYNDVAPFEVRLYKN 120  
 DB 61 KFGPLPSKQWQMASSEPPCVNKKVSDPKLEILLQNGLYLYIGQVAPNANYNDVAPFEVRLYKN 120  
 QY 121 KDMIQTLTKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPQFIS 177  
 DB 121 KDMIQTLTKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPQFIS 177

RESULT 4  
 Q80YG2 PRELIMINARY; PRT; 173 AA.

AC Q80YG2;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE GTR ligand.  
 GN Name="tnfsf18; Synonyms=tnfsf 18;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DBA/2J;  
 RA Bianchini R., Nocentini G., Ronchetti S., Ayroldi E., Riccardi C.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBA/Ca;  
 RX PubMed=14608036;  
 RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,  
 RA Waldmann H.;  
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is  
 RT costimulatory for T cells";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).  
 DR EMBL: AY343223; AAC09011.1; -  
 DR EMBL: AJ577579; CAB12166.1; -  
 DR EMBL: AJ577580; CAB12167.1; -  
 DR MGD: MGI:2673064; Tnfef18.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0005164; P:tumor necrosis factor receptor binding; IEA.  
 DR InterPro: IPR008983; TNF like.  
 DR InterPro: IPR003636; TNF subf.  
 DR ProDom: PD002012; TNF subf. 1.  
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 44.0%; Score 418.5; DB 2; Length 173;  
 Best Local Similarity 52.6%; Pred. No. 5.6e-31;

Matches 92; Conservative 20; Mismatches 58; Indels 5; Gaps 5;  
 QY 6 LEMPLSHRTGAGRSSWKMLFCSTVWLFICSPSWLIFFLQLETKAPECPMAKFGP 64  
 DB 1 MEMPLRESPPQRAERCK-KSWLLCTVALMLLCSGLTLYSLK-PTAIESCMVAFEL 58  
 QY 65 LPSKQWQMASSEPPCVNKKVSDPKLEILLQNGLYLYIGQVAP-NANY-NDVAPFEVRLYKNKD 122  
 DB 59 SSSKMHMTSPKPCVNTTSDGKLTILQSGTYLYIGQVTPYDKKIKONAPFVQIYKND 118  
 QY 123 MIOQLTKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPQFIS 177  
 DB 119 VLQTLNMDFOILPIGTYELHAGDNILYKFNKSDHIOKNNYWGIIILMDLPFIS 173

RESULT 5  
 CAE12167 PRELIMINARY; PRT; 173 AA.

AC CAE12167;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE GTR ligand.  
 GN TNFSF 18.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBA/Ca;  
 RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,  
 RA Waldmann H.;  
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is  
 RT costimulatory for T cells";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).  
 DR EMBL: AJ577579; CAB12166.1; -  
 KM Alternative splicing.  
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 44.0%; Score 418.5; DB 2; Length 173;  
 Best Local Similarity 52.6%; Pred. No. 5.6e-31;  
 Matches 92; Conservative 20; Mismatches 58; Indels 5; Gaps 5;

QY 6 LEMPLSHRTGAGRSSWKMLFCSTVWLFICSPSWLIFFLQLETKAPECPMAKFGP 64  
 DB 1 MEMPLRESPPQRAERCK-KSWLLCTVALMLLCSGLTLYSLK-PTAIESCMVAFEL 58  
 QY 65 LPSKQWQMASSEPPCVNKKVSDPKLEILLQNGLYLYIGQVAP-NANY-NDVAPFEVRLYKNKD 122  
 DB 59 SSSKMHMTSPKPCVNTTSDGKLTILQSGTYLYIGQVTPYDKKIKONAPFVQIYKND 118  
 QY 123 MIOQLTKSKIQNVGTYELHVGDTIDILFNSEHOVLKNNYWGIIILANPQFIS 177  
 DB 119 VLQTLNMDFOILPIGTYELHAGDNILYKFNKSDHIOKNNYWGIIILMDLPFIS 173

RESULT 6

CAE12167 PRELIMINARY; PRT; 173 AA.  
 AC CAE12167;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE GTR ligand.  
 GN TNFSF 18.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBA/Ca;

RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,  
 RA Waldmann H.;  
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is  
 RT costimulatory for T cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).  
 DR EMBL; AJ577580; CAB2167.1; -.  
 KM Alternative splicing.  
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 44.0%; Score 418.5; DB 2; Length 173;  
 Best Local Similarity 52.6%; Pred. No. 5,6e-31;  
 Matches 92; Conservative 20; Mismatches 58; Indels 5; Gaps 5;

QY 6 LENMPLSHSRTOGAORSSWKMLFCSIVMLL-FLCSFSLIFLQLETAKEPCNAKFGP 64  
 Db 1 MEEMPLRSPQRAERCK-KSWLCTIVALLMLLSTGLIYTSIK-PTVIESCWVKEFL 58  
 QY 65 LPSKQWASSEPPCNKVSMDKLEITLQNGLYLYGVAP-NANY-NDVAPFEVRLYKXND 122  
 Db 59 SSSKWHMSPKPHCVNTTSDGKTLQSGTYLYIGQVLPVDKXYIKDNAPEFVQYKXND 118  
 QY 123 MIQTLNKSQIONVGTIELHVGDTIDLFNSEHQLKNNYWGIIILANPOFIS 177  
 Db 119 VIQTLNMDFQLPLPGGVYELHAGDNITYLKFNKSKHIQKNTYWGIIIMPDLEFIS 173

## RESULT 7

QY 07TNY2 PRELIMINARY; PRT; 173 AA.  
 ID Q7TNY2;  
 AC Q7TNY2;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DB GTR ligand.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BAIB/c;  
 RX PubMed=14647196;  
 RA Kim J.D., Choi B.K., Bae J.S., Lee U.H., Han I.S., Lee H.W.,  
 RA Youn B.S., Vinay D.S., Kwon B.S.;  
 RT "Cloning and characterization of GTR ligand";  
 RL Genes Immun. 4:564-569(2003).  
 DR EMBL; AY267900; AAP96745.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; F:tumor necrosis factor receptor binding; IEA.  
 DR InterPro; IPR003636; TNF subf.  
 DR Prodom; PD002012; TNF subf. 1.  
 SQ SEQUENCE 173 AA; 19773 MW; 1FD22953BCFC34C5 CRC64;

Query Match 43.6%; Score 414.5; DB 2; Length 173;  
 Best Local Similarity 52.0%; Pred. No. 1,3e-30;  
 Matches 91; Conservative 20; Mismatches 59; Indels 5; Gaps 5;

QY 6 LENMPLSHSRTOGAORSSWKMLFCSIVMLL-FLCSFSLIFLQLETAKEPCNAKFGP 64  
 Db 1 MEEMPLRSPQRAERCK-KSWLCTIVALLMLLSTGLIYTSIK-PTVIESCWVKEFL 58  
 QY 65 LPSKQWASSEPPCNKVSMDKLEITLQNGLYLYGVAP-NANY-NDVAPFEVRLYKXND 122  
 Db 59 SSSKWHMSPKPHCVNTTSDGKTLQSGTYLYIGQVLPVDKXYIKDNAPEFVQYKXND 118  
 QY 123 MIQTLNKSQIONVGTIELHVGDTIDLFNSEHQLKNNYWGIIILANPOFIS 177  
 Db 119 VIQTLNMDFQLPLPGGVYELHAGDNITYLKFNKSKHIQKNTYWGIIIMPDLEFIS 173

## RESULT 8

Q7TS55

ID Q7TS55 PRELIMINARY; PRT; 173 AA.

AC Q7TS55;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE GTR ligand (glucocorticoid-induced-tumor necrosis factor receptor  
 DE ligand).  
 GN Name=Gitr1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57/BL6; TISSUE=spleen;  
 RA Ji H., Tenhore C.;  
 RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/J;  
 RX MEDLINE=22883945; PubMed=14521928;  
 RA Yu K.Y., Kim H.S., Song S.Y., Min S.S., Jeong J.J., Youn B.S.;  
 RT "Identification of a ligand for glucocorticoid-induced tumor necrosis  
 RT factor receptor constitutively expressed in dendritic cells.";  
 RL Biochem. Biophys. Res. Commun. 310:433-438(2003).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/J;  
 RA Yu K.-Y., Min S.S., Youn B.-S.;  
 RL Submitted (AUG-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY320040; AAP70494.1; -.  
 DR EMBL; AY359852; AA055265.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR003636; TNF subf.  
 DR Prodom; PD002012; TNF subf. 1.  
 KW Receptor.  
 SQ SEQUENCE 173 AA; 19732 MW; 0F08494CACF424D2 CRC64;

Query Match 43.4%; Score 412.5; DB 2; Length 173;  
 Best Local Similarity 52.0%; Pred. No. 2e-30;  
 Matches 91; Conservative 20; Mismatches 59; Indels 5; Gaps 5;

QY 6 LENMPLSHSRTOGAORSSWKMLFCSIVMLL-FLCSFSLIFLQLETAKEPCNAKFGP 64  
 Db 1 MEEMPLRSPQRAERCK-KSWLCTIVALLMLLSTGLIYTSIK-PTVIESCWVKEFL 58  
 QY 65 LPSKQWASSEPPCNKVSMDKLEITLQNGLYLYGVAP-NANY-NDVAPFEVRLYKXND 122  
 Db 59 SSSKWHMSPKPHCVNTTSDGKTLQSGTYLYIGQVLPVDKXYIKDNAPEFVQYKXND 118  
 QY 123 MIQTLNKSQIONVGTIELHVGDTIDLFNSEHQLKNNYWGIIILANPOFIS 177  
 Db 119 VIQTLNMDFQLPLPGGVYELHAGDNITYLKFNKSKHIQKNTYWGIIIMPDLEFIS 173

## RESULT 9

AA055265 PRELIMINARY; PRT; 173 AA.  
 ID AA055265;  
 AC AA055265;  
 DT 02-MAR-2004 (TREMBlrel. 27, Created)  
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)  
 DE Glucocorticoid-induced-tumor necrosis factor receptor ligand.  
 GN GTR1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.



RC STRAIN=129/1;  
RA MEDLINE=22883945; PubMed=14521928;  
RA Yu K.-Y., Kim H.-S., Song S.-Y., Min S.-S., Jeong J.-J., Yoon B.-S.;  
RT "Identification of a ligand for glucocorticoid-induced tumor necrosis  
RT factor receptor constitutively expressed in dendritic cells";  
RL Biochem. Biophys. Res. Commun. 310:433-438(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/1;  
RA Yu K.-Y., Min S.-S., Yoon B.-S.;  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY359852; AAG5265.1; -.  
KW Receptor.  
SQ SEQUENCE 173 AA; 19732 MW; 0F08494CACF424D2 CRC64;  
Query Match 43.4%; Score 412.5; DB 2; Length 173;  
Best Local Similarity 52.0%; Pred. No. 26-30;  
Matches 91; Conservative 20; Mismatches 59; Indels 5; Gaps 5;  
Db 6 LENMPLSHRTQGAQSSWMLFCSIWML-FLCSFSLIFLQLETAKEPCMAKFGP 64  
1 MEMPLRESSPQRAERCK-KSWMLCTVALLMLGSLGTLITSLK-PTAIESCWKFEI 58  
QY 65 LRSKMGMASSPPCVKVKVDKLEIIQNGLYLYGVAP-NANY-NDVAPFEVRLYKND 122  
Db 59 SSSKWMTPSPKPCVNTTSGKLLIQQSGTYLYGVVPIVDKXYIKDNPFFVQIYKND 118  
QY 123 MIOITLNKSKIQWVGTYELHVGDTIDLFNSEHOYLKNTTYGIIILANPQFIS 177  
Db 119 VQITLMDPQLIPGIVYELHAGDNIYLFKNSKDIQKNTTYGIIILMDPLPIS 173  
RESULT 10  
TNFS\_CHICK  
ID TNFS\_CHICK STANDARD; PRT; 272 AA.  
AC 091B8;  
DT 28-FEB-2003 (rel. 41, Created)  
DT 29-MAR-2004 (rel. 43, Last sequence update)  
DT 05-JUL-2004 (rel. 44, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-  
DE L) (CD154 protein).  
GN Name=TNFSF5; Synonyms=CD40LG, CD40L;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=White Leghorn; TISSUE=Spleen;  
RA Tregaskes C.A., Young J.R., Burnside J.;  
RT "Cloning of a putative chicken CD40 ligand."  
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell  
CC proliferation in the absence of co-stimulus as well as 198  
CC production in the presence of IL-4. Involved in immunoglobulin  
CC class switching (By similarity).  
CC -!- SUBUNIT: Homotrimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
CC extracellular soluble form (By similarity).  
CC -!- PTM: The soluble form derives from the membrane form by  
CC proteolytic processing (By similarity).  
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AJ243435; CAB95748.2; -.

DR HSP; P29965; 119R.  
DR GO; GO:0016021; C: integral to membrane; ISS.  
DR GO; GO:0005174; F: CD40 receptor binding; ISS.  
DR GO; GO:0042100; P: B-cell proliferation; ISS.  
DR GO; GO:0006954; P: inflammatory response; ISS.  
DR GO; GO:0007159; P: leukocyte cell adhesion; ISS.  
DR GO; GO:0030168; P: platelet activation; ISS.  
DR InterPro: IPR003263; TNF 5.  
DR InterPro: IPR006052; TNF family.  
DR InterPro: IPR008983; TNF-like.  
DR InterPro: IPR003636; TNF\_subf.  
DR Pfam: PF00229; TNF 1.  
DR PRINTS: PR01702; CD40LIGAND.  
DR ProDom: PD008600; TNF 5; 1.  
DR ProDom: PD002012; TNF\_subf. 1.  
DR PROSITE: PS00251; TNF 1; 1.  
DR PROSITE: PS00499; TNF 2; 1.  
KW Cytokine; Glycoprotein; Signal-anchor; Transmembrane.  
FT CHAIN 1 272  
FT Tumor necrosis factor ligand superfamily  
FT member 5, membrane form.  
FT CHAIN 111 272  
FT DOMAIN 1 23  
FT TRANSMEM 24 44  
FT SITE 45 272  
FT SITE 110 111  
FT DISULFID 190 229  
FT CARBOHYD 124 124  
FT CARBOHYD 146 146  
FT CARBOHYD 251 251  
SQ SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;  
Query Match 11.4%; Score 108.5; DB 1; Length 272;  
Best Local Similarity 29.8%; Pred. No. 0.08;  
Matches 36; Conservative 22; Mismatches 44; Indels 19; Gaps 5;  
Db 68 KMGMASSPPCVKVKVDKLEIIQNGLYLYGVAPNANYNDVAPFEVRLV----- 118  
153 KM-MTTSVPTSLSYHSGKLVKAGLYIYSQVSFCTKAASAFPTIYLYLYPMEE 211  
QY 119 -----KMKDMIOITLNKSKIQWVGTYELHVGDTIDLFNSEHOYLKNTTYGIIIL 169  
Db 212 DRLMKGLDTHSTALCELQSIREGVPELRQGDVFPVNVDTAVNVNPGTYGMFK 271  
QY 170 L 170  
Db 272 L 272

RESULT 11  
Q74LM5  
ID Q74LM5 PRELIMINARY; PRT; 273 AA.  
AC Q74LM5;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN OrderedCusNames=LJ0068;  
OS Lactobacillus johnsonii.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=33959;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=NCC 533;  
RA PubMed=14966310;  
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,  
RA Pitet A.-C., Zwielen M.-C., Rouvet M., Altermann F., Barrangou R.,  
RA Mollet B., Mercenier A., Klammer T., Arigoni F., Schell M.A.;  
RT "The genome sequence of the probiotic intestinal bacterium  
RT Lactobacillus johnsonii NCC 533";  
RT Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

DR EMBL; AE017200; AA08050.1; -  
KW Complete proteome; Hypoetical protein.  
SQ SEQUENCE 273 AA; 31108 MW; 34414AF96D1747A8 CRC64;  
Query Match 9.3%; Score 88.5; DB 2; Length 273;  
Best local Similarity 23.6%; Pred. No. 5.9;  
Matches 42; Conservative 32; Mismatches 47; Indels 57; Gaps 10;  
QY 27 WLFCSYVWLFCSFWSWLIFFLOLETAKEPCMAKFGELPSKQW---ASSEPPCVNKVS 83  
DB 8 WIF---LIVFVG---INIFLGIELWQPTLLSAGSTPQDTIKSETSDQITIPKVN 58  
QY 84 DWKLEILLONGYLL-----IYGVAPNANYNVA-----PEFVRLYKXKDM 123  
DB 59 DKQ---EDGYLLAAKNDSDWIKATQGVKQVNNSENLSVHLDKPTILSKXKKEAL 114  
QY 124 IQTLTKNSKIQNV--GGTY---ELHVGDTIDLIENSE-----HOVLKNN 162  
DB 115 REVWRPFKDSQNVYGVKNYTYLSLSESD--DYIFNQTKTKYGEPPAATARLHIIVKDN 170  
RESULT 12  
AA08050 PRELIMINARY; PRT; 273 AA.  
AC AA08050;  
DT 02-MAR-2004 (TREMblrel. 27, Created)  
DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)  
DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)  
DE Hypoetical protein.  
GN L70068.  
OS Lactobacillus johnsonii.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus  
OX NCBI\_TaxID=33959;  
RN [1]  
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RC STRAIN=NC 533;  
RX PubMed=14966310;  
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,  
Pitcec A.-C., Zehlen M.-C., Rouvel M., Altermann E., Barragou R.,  
Mollet B., Mercier A., Kleenhammer T., Arigoni F., Schell M.A.;  
RT "The genome sequence of the probiotic intestinal bacterium  
Lactobacillus johnsonii NC 533.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).  
DR EMBL; AE017200; AA08050.1; -  
KW Hypoetical protein.  
SQ SEQUENCE 273 AA; 31108 MW; 34414AF96D1747A8 CRC64;  
Query Match 9.3%; Score 88.5; DB 2; Length 273;  
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QY 27 WLFCSYVWLFCSFWSWLIFFLOLETAKEPCMAKFGELPSKQW---ASSEPPCVNKVS 83  
DB 8 WIF---LIVFVG---INIFLGIELWQPTLLSAGSTPQDTIKSETSDQITIPKVN 58  
QY 84 DWKLEILLONGYLL-----IYGVAPNANYNVA-----PEFVRLYKXKDM 123  
DB 59 DKQ---EDGYLLAAKNDSDWIKATQGVKQVNNSENLSVHLDKPTILSKXKKEAL 114  
QY 124 IQTLTKNSKIQNV--GGTY---ELHVGDTIDLIENSE-----HOVLKNN 162  
DB 115 REVWRPFKDSQNVYGVKNYTYLSLSESD--DYIFNQTKTKYGEPPAATARLHIIVKDN 170  
RESULT 13  
0861B8 PRELIMINARY; PRT; 516 AA.  
AC 0861B8;  
DT 01-JUN-2003 (TREMblrel. 24, Created)  
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
DE Hypoetical protein.

OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RX MEDLINE=22092622; PubMed=12097910;  
RA Gloeener G., Richinger L., Szafrenki K., Pachebat J., Dear P.,  
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,  
Tunggal B., Cox B., Quail M.A., Platzer W., Rosenthal A., Noegel A.A.;  
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";  
RL Nature 418:79-85(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RA Baumgart C.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC116511; AA052204.1; -  
KW Hypoetical protein.  
SQ SEQUENCE 516 AA; 58667 MW; 80B308CF6CDF97C2 CRC64;  
Query Match 9.1%; Score 86.5; DB 2; Length 516;  
Best local Similarity 29.0%; Pred. No. 19;  
Matches 27; Conservative 17; Mismatches 36; Indels 13; Gaps 3;  
QY 80 NKVSDWKLLEILLONGYLLIYGVAPNANYNVAPFEVRLYKXKDMIQTLTKNSKIQNVGGT 139  
DB 419 NETDSDKLT-----IYIY-----NIKQDVPQVTFVIEFKDEINEMITKHFQIENNDS 469  
QY 140 YELHVGDTIDLIENSEHOVLKNNYGIILLAN 172  
DB 470 VNNINNEKNDPILN---IPDGNCDGIILLTN 498  
RESULT 14  
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AC 0896D6;  
DT 01-JUN-2003 (TREMblrel. 24, Created)  
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
DE K11A protein, putative phage-related DNA binding protein.  
GN Name=K11A; Order=docuNames=CTC01071;  
OS Clostridium tetani.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Massachusetts / E88;  
RX MEDLINE=22457253; PubMed=12552129;  
RA Brueggemann H., Baewer S., Fricke W.F., Wietzer A., Liesegang H.,  
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,  
Goetschalck G.;  
RT "The genome sequence of Clostridium tetani, the causative agent of  
tetanus disease.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).  
DR EMBL; AE015939; AA035654.1; -  
DR InterPro; IPR003497; BRO\_N.  
DR Pfam; PF02498; Bro-N; 1.  
KW Complete proteome.  
SQ SEQUENCE 270 AA; 31533 MW; C378AB524C0133A8 CRC64;  
Query Match 9.0%; Score 85.5; DB 2; Length 270;  
Best local Similarity 25.4%; Pred. No. 11;  
Matches 31; Conservative 18; Mismatches 36; Indels 37; Gaps 5;  
QY 81 KVSDWKLLEILLONGYLLIYGVAPNANYNVAPFEVRLYKXKDMIQTLTKNSKIQNVGGT 139  
DB 134 KAKKMLEILLONGYLLIYGVAPNANYNVAPFEVRLYKXKDMIQTLTKNSKIQNVGGT 186  
QY 140 -----YELHVG-----DTIDLIENSEHOVLKNNYV---GIILL 170

DB 187 LINKLHEKVOYQNDQWMLYKESGKGYTHSETIDIVRSDBGPDVYKMTKTKQGRLEL 246  
 QY 171 AN 172  
 DB 247 YN 248

RESULT 15  
 MLC1 HUMAN STANDARD: PRT; 376 AA.  
 AC 015049; ORTAGS: G96RPS; G9UG8;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Membrane protein MLC1.  
 GN Name=MLC1; Synonyms=WKL1, KIAA0027;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
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 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=96051387; PubMed=7584026;  
 RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,  
 RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;  
 RT "Prediction of the coding sequences of unidentified human genes. I.  
 RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  
 RT analysis of randomly sampled cDNA clones from human immature myeloid  
 RT cell line KG-1.";  
 RL DNA Res. 1:27-35(1994).  
 [2]  
 RP REVISIONS.  
 RX MEDLINE=22158633; PubMed=12168954;  
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual  
 RT curation of 330 KIAA cDNA clones.";  
 RL DNA Res. 9:99-106(2002).  
 [3]  
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANT PC MET-308.  
 RC TISSUE=Hippocampus;  
 RX MEDLINE=21255990; PubMed=11326298; DOI=10.1038/sj/mp/4000869;  
 RA Meyer U., Huberth A., Ortega G., Sygallio Y.V., Jatzke S.,  
 RA Moesner R., Strom T.M., Ulzheimer-Teuber I., Szeceger G., Schmitt A.,  
 RA Lesch K.P.;  
 RT "A missense mutation in a novel gene encoding a putative cation  
 RT channel is associated with catatonic schizophrenia in a large  
 RT pedigree.";  
 RL Mol. Psychiatry 6:302-306(2001).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;  
 RA Dunham I., Hunt A.R., Collins J.E., Buskiewicz R., Beare D.M.,  
 RA Clamp M., Smith L.J., Ainscough R., Almeida J.P., Babage A.K.,  
 RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,  
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
 RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
 RA Gilbert J.G.R., Goward M.E., Graffam D.V., Griffiths M.N.D., Hall C.,  
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
 RA Laid G.K., Langford C.F., Leversha M.A., Lloyd D.M., Lloyd D.M.,  
 RA Maryn I.D., Mashneghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
 RA Mcclay J., McLaren S., McMurtry A.A., Milne S.A., Mortimore B.J.,  
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Rose M.T.,  
 RA Scott C.E., Sehra H.K., Skuse C.D., Smalley S., Smith M.L.,  
 RA Soderlund C., Spraggon L., Stewart C.A., Sulston J.E., Swann R.M.,  
 RA Vaudin M., Wallis J., Wallis J.M., Whiteley M.N., Willey D.L.,  
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,  
 RA Roe B.A., Chen F., Chu L., Crabtree J., Aoki N., Mitsuyama S.,  
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Mink P.,  
 RA Fullon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
 RA Hinds K., Kemp K., Lettreille P., Layman D., Ozersky P., Rohlfing T.,  
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,  
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,  
 RA Wilson R., Emanuel B.S., Shaikh T., Kurashiki H., Saita S.,  
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
 RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,  
 RA O'Brien K.P., Wilkinson P., Bodenreich A., Hartman K., Hu X.,  
 RA Khan A.S., Lane L., Tiliakou Y., Wright H.;  
 RT "The DNA sequence of human chromosome 22.";  
 RL Nature 402:489-495(1999).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Utislid T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Millar S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [6]  
 RP SEQUENCE OF 1-13.  
 RC TISSUE=Platelet;  
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;  
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,  
 RA Thomas G.R., Vandekerckhove J.;  
 RT "Exploring proteomes and analyzing protein processing by mass  
 RT spectrometric identification of sorted N-terminal peptides.";  
 RL Nat. Biotechnol. 21:566-569(2003).  
 [7]  
 RP VARIANTS MLC LEU-92; ARG-117; ARG-211 AND LEU-279.  
 RX MEDLINE=21152271; PubMed=11254442;  
 RA Leegwater P.A.J., Yuan B.Q., van der Steen J., Mulders J.,  
 RA Koenst A.A.M., Ijla Boor P.K., Mejaski-Bosnjak V.,  
 RA van der Maarel S.M., Frants R.R., Oudejans C.B.M., Schutgens R.B.H.,  
 RA Pronk J.C., van der Knapp M.S.;  
 RT "Mutations of MLC1 (KIAA0027), encoding a putative membrane protein,  
 RT cause megalencephalic leukoencephalopathy with subcortical cysts.";  
 RL Am. J. Hum. Genet. 68:831-838(2001).  
 [8]  
 RP VARIANTS MLC SER-91; LYS-140 AND SER-140.  
 RX PubMed=11935341; DOI=10.1007/s00439-002-0682-x;  
 RA Leegwater P.A.J., Boor P.K.I., Yuan B.Q., van der Steen J., Visser A.,  
 RA Konst A.A.M., Oudejans C.B.M., Schutgens R.B.H., Pronk J.C.,  
 RA van der Knapp M.S.;  
 RT "Identification of novel mutations in MLC1 responsible for  
 RT megalencephalic leukoencephalopathy with subcortical cysts.";

RL Hum. Genet. 110:279-283 (2002).  
RN [9]  
RP VARIANT MLC GLD-58.  
RX PubMed=12189496; DOI=10.1007/s00439-002-0770-Y;  
RA Ben-Zeev B., Levy-Nissenbaum E., Lahat H., Ankster Y., Shinar Y.,  
RA Brand N., Goss-Tzur V., Macgregor D., Sidi R., Kleit R., Frydman M.,  
RA Pras E.;  
RT "Megalencephalic leukoencephalopathy with subcortical cysts: a founder  
effect in Israeli patients and a higher than expected carrier rate  
among Libyan Jews.";  
RT Hum. Genet. 111:214-218 (2002).  
CC -1- FUNCTION: May be a transporter. May act as a non-selective  
CC neuronal cation channel.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: Expressed in the brain, with highest levels  
CC found in the amygdala, nucleus caudatus, thalamus and hippocampus.  
CC -1- DISEASE: Defects in MLC1 are a cause of megalencephalic  
CC leukoencephalopathy with subcortical cysts (MLC) [MIM:604004]. MLC  
CC is an autosomal recessive disorder characterized by macrocephaly,  
CC deterioration of motor functions with ataxia, and spasticity,  
CC eventuating in mental decline. The brain appears swollen on  
CC magnetic resonance imaging, with diffuse white-matter  
CC abnormalities and the invariable presence of subcortical cysts.  
CC -1- DISEASE: Defects in MLC1 are a cause of periodic cataplexia (PC), a  
CC familial subtype of cataplexia schizophrenia which is a genetically  
CC heterogeneous disorder characterized by psychosis and psychomotor  
CC disturbances.  
CC -----  
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CC -----  
DR EMBL; D25217; BAA04947.3; ALT\_INIT.  
DR EMBL; AF119633; AAK60119.1; -;  
DR EMBL; AL022327; CAB51559.1; ALT\_INIT.  
DR EMBL; BC028425; AAB8425.1; -;  
DR Genew; HGNC:17082; MLC1.  
DR MIM; 605908; -;  
DR MIM; 604004; -;  
DR GO; GO:0000299; C:integral to membrane of membrane fraction; TAS.  
KW Direct protein sequencing; Disease mutation; Ionic channel;  
KW Transmembrane; Transport.  
KW INIT MET 0  
FT TRANSSEM 55 71 Potential.  
FT TRANSSEM 112 127 Potential.  
FT TRANSSEM 145 161 Potential.  
FT TRANSSEM 199 215 Potential.  
FT TRANSSEM 227 243 Potential.  
FT TRANSSEM 301 317 Potential.  
FT DOMAIN 261 279 Pore-region (Potential).  
FT DOMAIN 172 175 Poly-Lys.  
FT VARIANT 58 58 G -> E (in MLC).  
FT VARIANT 91 91 P -> S (in MLC).  
FT VARIANT 92 92 /FTid=VAR\_017439.  
FT VARIANT 117 117 S -> L (in MLC).  
FT VARIANT 117 117 /FTid=VAR\_011699.  
FT VARIANT 117 117 T -> R (in MLC).  
FT VARIANT 117 117 /FTid=VAR\_011700.

Query Match 9.0%; Score 85.5; DB 1; Length 376;  
Best local similarity 20.8%; Pred. No. 16;  
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DB 126 IFPGCKVLNDSAININENLILLLLELLMAATVITA-----ARSSSEDCKKK-- 173  
QY 84 DWKLEIIIONGILYLGVA PANANVDVAPFEVRLYKNKDMIQTLNKSQIONVGTYELH 143

DB 174 -----KSSMSD SANILDEVPFPAVLKSYVEVYAGISAV--LGIIILAN 217  
QY 144 VGPITDIENSEHQVLKNTYRGIIILANQFIS 177  
DB 218 VDDSV---SGPHLSV---TFWILVACFPSAIA 244

Search completed: November 2, 2004, 12:40:57  
Job time : 196 secs



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XX      Yu G, Ni J, Rosen CA;
XX      WPI; 1998-169182/15.
XX      N-PSDB; AAV19195.
XX      Nucleic acid encoding human endokine-alpha - useful for diagnosis and
XX      treatment of tumour necrosis factor-related diseases.
XX      Claim 1; Fig 1A-B; 78bp; English.
XX
XX      This polypeptide comprises human endokine-alpha, a novel member of the
XX      tumour necrosis factor (TNF) family of cytokines that shows 30%
XX      similarity and 22% identity to human TNF-alpha. Its amino acid sequence
XX      was deduced from a human striatum cDNA clone (see AAV19195). Isolation of
XX      this nucleic acid allows production of recombinant endokine-alpha
XX      polypeptides in transformed host cells. Endokine-alpha may be involved in
XX      disorders of immunomodulation, infection, cell proliferation,
XX      angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxaemia, and
XX      may be useful for treating melanoma and sarcoma, particularly where
XX      coupled to a radioisotope or cytostatic agent. Antibodies raised against
XX      endokine-alpha are useful diagnostically and for treatment of TNF-
XX      associated disease
XX
XX      Sequence 169 AA;
XX
XX      Query Match      100.0%; Score 675; DB 2; Length 169;
XX      Best Local Similarity 100.0%; Pred. No. 2.2e-69;
XX      Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1  ETAKPCCAKRGPPPSKQWASSEPPCVNKYSMDKLELTONGLYLIYQVAPNANYNDVA 60
XX      DB      44  ETAKPCCAKRGPPPSKQWASSEPPCVNKYSMDKLELTONGLYLIYQVAPNANYNDVA 103
XX      QY      61  PFEVRLYLNKMKMIQTLTNKSKIQNVGGTYELHVGPTIDLIENSEHOVLKNTYWGIIILA 120
XX      DB      104  PFEVRLYLNKMKMIQTLTNKSKIQNVGGTYELHVGPTIDLIENSEHOVLKNTYWGIIILA 163
XX      QY      121  NPQRTIS 126
XX      DB      164  NPQRTIS 169
XX
XX      RESULT 2
XX      ID      AAB08785 standard; protein; 169 AA.
XX      AC      AAB08785;
XX      DT      02-JAN-2001 (first entry)
XX
XX      A human endokine-alpha polypeptide.
XX
XX      Human; endokine-alpha; cytokine; tumour necrosis factor; TNF; AIDS;
XX      chronic lymphocyte disorder; tumour; parasitic disease; arthritis;
XX      autoimmune disease; lupus; multiple sclerosis; chronic inflammation;
XX      acute inflammation; acute allograft rejection; graft versus host disease;
XX      transplant rejection; foetal resorption; faecal peritonitis; allergy;
XX      bowel disease; sepsis; leukaemia; chronic hypergammaglobulinemia;
XX      polychondritis; scleroderma; Wegener granulomatosis; dermatomyositis;
XX      chronic active hepatitis; myasthenia gravis; psoriasis; vitiligo;
XX      Steven-Johnson syndrome; idiopathic sprue; gluten-sensitive enteropathy;
XX      pemphigus vulgaris; Goodpasture's disease; bullous pemphigoid;
XX      discoid lupus; dense deposit disease; endocrine ophthalmopathy;
XX      irritable bowel disease; asthma; Grave's disease; sarcoidosis; cirrhosis;
XX      juvenile diabetes; insulin dependent diabetes mellitus; uveitis;
XX      lymphopenias; polyarteritis nodosa; Sjogren's syndrome; Bechet's disease;
XX      primary myxedema; polymyositis; mixed connective tissue disease;
XX      keratoconjunctivitis sicca; vernal keratoconjunctivitis, ss.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers

```

```

FT      Domain      1..17
FT      /note= "intracellular domain"
FT      Domain      18..43
FT      /note= "transmembrane domain"
FT      Domain      44..169
FT      /note= "extracellular domain"
XX
XX      WO200050620-A2.
XX
XX      31-AUG-2000.
XX
XX      25-FEB-2000; 2000WO-US004722.
XX
XX      26-FEB-1999; 99US-0122099P.
XX      28-MAY-1999; 99US-0136788P.
XX      (HUMA-) HUMAN GENOME SCI INC.
XX
XX      Yu G, Ni J, Rosen CA;
XX      WPI; 2000-572097/53.
XX      N-PSDB; AAA74936.
XX
XX      Polynucleotide encoding endokine alpha protein, which is a member of
XX      tumor necrosis factor useful for treating inflammatory diseases,
XX      disorders such as cancer, allergy, diabetes and various neurological
XX      disorders.
XX
XX      Claim 16; Fig 1; 263pp; English.
XX
XX      The present sequence represents a human endokine-alpha polypeptide. The
XX      polypeptide is a cytokine which is similar to tumour necrosis factor
XX      (TNF). The endokine-alpha polynucleotides and polypeptides are useful for
XX      treating AIDS, chronic lymphocyte disorder, tumours, parasitic disease,
XX      autoimmune disease, lupus, arthritis, multiple sclerosis, chronic
XX      inflammation, acute inflammation, acute allograft rejection, graft versus
XX      host disease, transplant rejection, foetal resorption, faecal
XX      peritonitis, skin allergies, bowel disease, sepsis, leukaemia, chronic
XX      hypergammaglobulinemia, polychondritis, scleroderma, Wegener
XX      granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia
XX      gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, vitiligo,
XX      gluten-sensitive enteropathy, pemphigus vulgaris, Goodpasture's disease,
XX      bullous pemphigoid, discoid lupus, dense deposit disease, endocrine
XX      ophthalmopathy, irritable bowel disease, asthma, Grave's disease,
XX      sarcoidosis, cirrhosis, juvenile diabetes, insulin dependent diabetes
XX      mellitus, uveitis, lymphopenias, polyarteritis nodosa, Sjogren's
XX      syndrome, Bechet's disease, primary myxedema, polymyositis, mixed
XX      connective tissue disease, keratoconjunctivitis sicca, and vernal
XX      keratoconjunctivitis,
XX
XX      Sequence 169 AA;
XX
XX      Query Match      100.0%; Score 675; DB 3; Length 169;
XX      Best Local Similarity 100.0%; Pred. No. 2.2e-69;
XX      Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1  ETAKPCCAKRGPPPSKQWASSEPPCVNKYSMDKLELTONGLYLIYQVAPNANYNDVA 60
XX      DB      44  ETAKPCCAKRGPPPSKQWASSEPPCVNKYSMDKLELTONGLYLIYQVAPNANYNDVA 103
XX      QY      61  PFEVRLYLNKMKMIQTLTNKSKIQNVGGTYELHVGPTIDLIENSEHOVLKNTYWGIIILA 120
XX      DB      104  PFEVRLYLNKMKMIQTLTNKSKIQNVGGTYELHVGPTIDLIENSEHOVLKNTYWGIIILA 163
XX      QY      121  NPQRTIS 126
XX      DB      164  NPQRTIS 169
XX
XX      RESULT 3
XX      ID      AAY53061 standard; protein; 169 AA.
XX

```

```

AC AAY53061;
XX
XX 03-APR-2000 (first entry)
XX
XX
DE Human endokine alpha protein SEQ ID NO:2.
XX
XX Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
KW immunomodulation; inflammation; cell proliferation; angiogenesis;
XX tumour metastasis; apoptosis; sepsis; endotoxemia.
XX
OS Homo sapiens.
XX
XX US5998171-A.
XX
XX 07-DEC-1999.
XX
XX 15-AUG-1997; 97US-00912227.
XX
XX 16-AUG-1996; 96US-0024058P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX NI J, Rosen CA, Yu G;
XX
XX WPI; 2000-104608/09.
XX
XX N-PSDB; AAZ57314.
XX
XX Isolated human endokine alpha gene useful as a diagnostic probes and
PT primers.
XX
XX Claim 1; Fig 1; 31pp; English.
XX
XX The present sequence represents human endokine alpha which is a member of
CC the tumour necrosis factor (TNF) family of cytokines. Endokine alpha
CC protein and polynucleotides can be used in diagnostic and therapeutic
CC methods concerning TNF family-related disorders. These include disorders
CC associated with immunomodulation and inflammation, cell proliferation,
CC angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxemia
XX
XX Sequence 169 AA;
SQ
Query Match 100.0%; Score 675; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.2e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETAKPECPMAKFGPLPSKQWASSEPPCVNKNVSDMKLEITLNGXYLYIGVAPNANNVDVA 60
DB 44 ETAKPECPMAKFGPLPSKQWASSEPPCVNKNVSDMKLEITLNGXYLYIGVAPNANNVDVA 103
QY 61 PFEVRLYKNKDMITQTLTNKSKIQNVGTYELHVGDTIDLI FNSBHQVLKNNYWGIIILLA 120
DB 104 PFEVRLYKNKDMITQTLTNKSKIQNVGTYELHVGDTIDLI FNSBHQVLKNNYWGIIILLA 163
QY 121 NPOQFIS 126
DB 164 NPOQFIS 169

```

RESULT 4  
ADAI1464  
ID ADAI1464 standard; protein; 169 AA.

AC ADAI1464;

XX 06-NOV-2003 (first entry)

XX Human endokine alpha.

XX human; endokine alpha; melanoma; sarcoma; tumour; tumour regression;  
KM infection; viral; bacterial; yeast; fungal; toxoplasma gondii;  
KM Schistosoma mansoni; listeria monocytogenes; tumour necrosis factor;  
KM TNF-related disorder; endokine alpha-related disorder; immunomodulation;  
KM inflammation; cell proliferation; angiogenesis; tumour metastasis;

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KM apoptosis; sepsis; endotoxaemia.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Domain 1..17
XX Domain /label = Intracellular_domain
XX Domain 18..43
XX Domain /label = Transmembrane_domain
XX Domain 44..169
XX Domain /label = Extracellular_domain
XX
XX US2002099198-A1.
XX
XX 25-JUL-2002.
XX
XX 01-JUL-1999; 99US-00345790.
XX
XX 16-AUG-1996; 96US-0024058P.
XX
XX 15-AUG-1997; 97US-00912227.
XX
XX (YUGG/) YU G.
XX PA (NIJU/) NI J.
XX PA (ROSE/) ROSEN C A.
XX
XX YU G, NI J, Rosen CA;
XX
XX WPI; 2003-605663/57.
XX
XX N-PSDB; ADAI1463.
XX
XX Novel isolated endokine alpha polypeptide, a member of tumor necrosis
PT factor ligand family, and antibodies against the polypeptides, useful for
PT treating melanoma, sarcoma, and viral, bacterial, fungal infections.
XX
XX Claim 16; Fig 1; 29pp; English.
XX
XX The invention relates to an isolated human endokine alpha polypeptide. A
CC cell recombinant for the human endokine alpha polypeptide is useful for
CC producing the protein by recombinant techniques. The antigenic epitope
CC bearing peptides and polypeptides are useful to raise antibodies
CC including monoclonal antibodies. The peptides and antipeptide antibodies
CC are used in a variety of qualitative or quantitative assays for the
CC protein. The protein is useful for tumour targeting and thus used in
CC patients with melanoma and sarcoma for tumour regression and extension of
CC patient life-span through a local injection. The protein is also useful
CC for treating viral, bacterial, yeast, fungal and other infections e.g.,
CC toxoplasma gondii, Schistosoma mansoni, listeria monocytogenes etc. The
CC protein is also useful for treating other tumour necrosis factor (TNF)-
CC related disorders. The nucleic acid is useful as probes for gene mapping
CC by in situ hybridisation and for detecting expression of endokine alpha
CC gene in human tissue e.g. by Northern blot analysis. The nucleic acid is
CC also useful for diagnosing an endokine alpha-related disorder such as
CC disorders associated with immunomodulation and inflammation, cell
CC proliferation, angiogenesis, tumour metastasis, apoptosis, sepsis or
CC endotoxaemia. The antibody is useful diagnostically or therapeutically as
CC antagonists in the treatment of alpha and/or TNF-related disorders. The
CC antibody is also useful for purification of the protein. The antibodies
CC are useful for detecting the protein and for tracking the fate of various
CC regions of a protein precursor which undergoes post-translational
CC processing. The present sequence represents the amino acid sequence of
CC human endokine alpha.
XX
XX Sequence 169 AA;
SQ
Query Match 100.0%; Score 675; DB 6; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.2e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETAKPECPMAKFGPLPSKQWASSEPPCVNKNVSDMKLEITLNGXYLYIGVAPNANNVDVA 60
DB 44 ETAKPECPMAKFGPLPSKQWASSEPPCVNKNVSDMKLEITLNGXYLYIGVAPNANNVDVA 103
QY 61 PFEVRLYKNKDMITQTLTNKSKIQNVGTYELHVGDTIDLI FNSBHQVLKNNYWGIIILLA 120

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Db      104 PFEVRLYNKQKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHQVAKNTYWGIIILIA 163
QY      121 NPQFIS 126
      |||||
Db      164 NPQFIS 169

RESULT 5
ADCC01858
ID      ADCC01858 standard; protein; 169 AA.
XX
XX      ADCC01858;
AC
XX      18-DEC-2003 (first entry)
DT
XX
XX      Human Endokine alpha.
DE
XX      Human; endokine alpha; tumour necrosis factor family; AIDS;
KW      chronic lymphocyte disorder; tumour; parasitic disease;
KW      autoimmune disease; lupus; arthritis; multiple sclerosis; inflammation;
KW      graft versus host disease; transplant rejection; skin allergy;
KW      bowel disease; wound; sepsis; Hodgkin's disease;
KW      chronic lymphocyte leukaemia; Burkitt's lymphoma; scleroderma;
KW      chronic active hepatitis; myasthenia gravis; psoriasis;
KW      autoimmune thyroiditis; Goodpasture's disease; asthma; Graves disease;
KW      celiac disease; insulin dependent diabetes mellitus; Sjogren's syndrome;
KW      glomerulonephritis; hepatitis; Parkinson's disease; atherosclerosis;
KW      rheumatoid arthritis.
XX
XX      Homo sapiens.
OS
XX
XX      Key      Location/Qualifiers
FH      Protein      2..169
FT      /note= "This protein is specifically claimed in claim 11"

US2002168729-A1.
PD      14-NOV-2002.
XX
XX      02-MAY-2002; 2002US-00136511.
PF
XX      16-AUG-1996; 96US-0024058P.
PR
XX      15-AUG-1997; 97US-0031222Z.
PR      26-FEB-1999; 99US-0120999P.
PR      28-MAY-1999; 99US-0136788P.
PR      01-JUL-1999; 99US-00345790.
PR      25-FEB-2000; 2000US-00513584.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
PA
XX      Yu G, Ni J, Rosen CA;
PI
XX      WPI; 2003-755028/71.
DR      N-PSDB; ADCC01857.
XX
XX      Novel isolated endokine alpha polypeptide A1DS, chronic lymphocyte
PT      disorder, common variable immunodeficiency, a tumor, parasitic disease,
PT      autoimmune disease, lupus, arthritis, multiple sclerosis.
XX
XX      Claim 11; SEQ ID NO 2; 90pp; English.
XX
XX      The invention relates to an isolated endokine alpha polypeptide (a member
CC      of the tumour necrosis factor family), appearing as ADCC01858, the
CC      sequence of the endokine alpha polypeptide having an sequence encoded by
CC      the cDNA clone contained in ATCC Deposit number 97640 (A1) and the
CC      sequence of an epitope-bearing portion of the above polypeptides. Also
CC      included are the encoding nucleic acid (its homologues, complements or
CC      fragments where the fragment comprises at least 50 contiguous
CC      nucleotides), provided that the fragment is not from a region starting at
CC      nucleotide 26 and ending at nucleotide 476 of ADCC01857), making a
CC      recombinant vector comprising the nucleic acid and an isolated antibody
CC      or antibody fragment that binds specifically to endokine alpha. The DNA

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CC      and protein are useful for treating an individual having a disorder
CC      chosen from AIDS, chronic lymphocyte disorder, common variable
CC      immunodeficiency, a tumour, parasitic disease, autoimmune disease, lupus,
CC      arthritis, idiopathic thrombocytopenic purpura, multiple sclerosis,
CC      chronic inflammation, acute inflammation, acute allograft rejection,
CC      graft versus host disease, transplant rejection, foetal resorption,
CC      faecal peritonitis, skin allergies, bowel disease, a wound, sepsis, A1U,
CC      Hodgkin's disease, non-Hodgkin's lymphoma, chronic lymphocyte leukaemia,
CC      plasmacytoma, multiple myeloma, Burkitt's lymphoma, EBV-transformed
CC      disease, chronic myelogenous leukaemia, chronic hypergammaglobulinaemia,
CC      autoimmune haematological disorders, polychondritis, scleroderma, Wegener
CC      granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia
CC      gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, autoimmune
CC      thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive
CC      enteropathy, autoimmune neutropenia, pemphigus vulgaris, Goodpasture's
CC      disease, bullous pemphigoid, discoid lupus, dense deposit disease,
CC      endocrine ophthalmopathy, IBD, asthma, Graves disease, Sarcoidosis,
CC      cirrhosis, juvenile diabetes, insulin dependent diabetes mellitus,
CC      uveitis, autoimmune gastritis, lymphopoenia, olatertitis nodosa,
CC      Sjogren's syndrome, Behcet's disease, Hashimoto's disease, primary
CC      myxedema, polyomyelitis, mixed connective tissue disease, primary
CC      keratoconjunctivitis sicca, vernal keratoconjunctivitis, interstitial
CC      lung fibrosis, glomerulonephritis, hepatitis, autoimmune haemolytic
CC      anaemia, contact sensitivity disease, Parkinson's disease, primary
CC      lateral sclerosis, siliocosis, sarcoidosis, idiopathic pulmonary fibrosis,
CC      idiopathic hyper-eosinophilic syndrome, endotoxic shock, atherosclerosis,
CC      histamine-mediated allergic reactions, Ige-mediated allergic reactions,
CC      rheumatoid arthritis, plastic anaemia and myelodysplastic syndrome. The
CC      present sequence represents endokine alpha.
XX
XX      Sequence 169 AA;
SQ
XX
XX      Query Match      100.0%; Score 675; DB 7; Length 169;
XX      Best Local Similarity 100.0%; Pred. No. 2.2e-69;
XX      Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EFAKPPCAKFGPLPSKQWMASSPPCVNKVSDMKLEILQNGLYIGQVAPNANYNVA 60
      |||||
Db      44 EFAKPPCAKFGPLPSKQWMASSPPCVNKVSDMKLEILQNGLYIGQVAPNANYNVA 103
      |||||
QY      61 PFEVRLYNKQKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHQVAKNTYWGIIILIA 120
      |||||
Db      104 PFEVRLYNKQKMIQTLTNKSKIQNVGTYELHVGDTIDLIENSEHQVAKNTYWGIIILIA 163
      |||||
QY      121 NPQFIS 126
      |||||
Db      164 NPQFIS 169

RESULT 6
AAV15817
ID      AAV15817 standard; protein; 177 AA.
XX
XX      AAV15817;
AC
XX      28-JUL-1999 (first entry)
DT
XX
XX      Amino acid sequence of human DNA19355 polypeptide.
DE
XX
XX      DNA19355; tumour necrosis factor homologue; receptor G1TR; immunogen;
KW      antibody; apoptosis; mammalian cancer cell;
KW      tumour necrosis factor (TNF)-alpha secretion; primary T- cell;
KW      proinflammatory response.
XX
XX      Homo sapiens.
OS
XX      MO9925834-A1.
PN      WO9925834-A1.
XX
XX      27-MAY-1999.
PD
XX      18-NOV-1998; 98WO-US024621.
PF      18-NOV-1997; 97US-0065635P.
XX
XX      18-NOV-1997; 97US-0065635P.

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PR 12-DEC-1997; 97US-0069661P.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Gurney AL, Marsters SA, Pitti R, Baker KP,
XX Godowski PJ, Mark MR;
XX WPI; 1999-338009/28.
XX N-PSDB; AAX59744.
XX
XX New DNA19355 polypeptide as tumour necrosis factor homolog.
XX
XX Claim 10; Fig 1; 86pp; English.
XX
XX The present sequence represents a polypeptide designated DNA19355. The
XX polypeptide is a tumour necrosis factor homologue. The DNA19355
XX polynucleotide sequence can be used to derive hybridisation probes for
XX e.g. isolating similar sequences, gene mapping, genetic analysis, etc.
XX Nucleic acids which encode DNA19355 can also be used to generate
XX transgenic or knockout animals, which are useful in the development and
XX screening of therapeutically useful reagents. The DNA19355 polypeptides
XX may be used in diagnostic assays to detect the presence of the receptor
XX GTR in mammalian tissues. The polypeptides can also be used as
XX immunogens to raise antibodies. The polypeptides may also be used to
XX induce apoptosis in mammalian cancer cells. DNA19355 polypeptides
XX stimulate secretion of tumour necrosis factor (TNF)-alpha in primary T-
XX cells, and so can be used to stimulate a proinflammatory response in
XX mammalian cells
XX
XX Sequence 177 AA:
SQ
Query Match 100.0%; Score 675; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.4e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIAKEPCMAKFGPLPSKQWQASSEPPCVNKVSDMKLEILLONGLYLYGGVAPANANDVA 60
DB 52 EIAKEPCMAKFGPLPSKQWQASSEPPCVNKVSDMKLEILLONGLYLYGGVAPANANDVA 111
QY 61 PFEVRLYKKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIENSEHOVLKNNYTWGIIILA 120
DB 112 PFEVRLYKKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIENSEHOVLKNNYTWGIIILA 171
QY 121 NPOFIS 126
DB 172 NPOFIS 177
RESULT 7
AAY06646
XX AAY06646 standard; protein; 177 AA.
XX
XX AAY06646;
XX
XX 26-OCT-1999 (first entry)
XX
XX Human PRO364 ligand.
XX
XX PRO364 ligand; tumour necrosis factor receptor; human; apoptosis;
XX inflammation; antiinflammatory; NF-KB activation; autoimmune disease;
XX therapy.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Domain 1..25 "cytoplasmic domain"
XX Domain 26..51
XX Domain /note="transmembrane domain"
XX Domain 52..177
XX Domain /note="extracellular domain"
XX Modified-site 129
XX /note="N-glycosylation"

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FT Modified-site 161
FT /note="N-glycosylation"
XX
XX W09940196-A1.
XX
XX 12-AUG-1999.
XX
XX 09-FEB-1999; 99MO-US0002642.
XX
XX 09-FEB-1998; 98US-0074087P.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Gurney AL, Marsters SA, Pitti RM, Wood WT,
XX Goddard A;
XX WPI; 1999-494296/41.
XX N-PSDB; AAX87726.
XX
XX Tumor necrosis factor receptor homologue - useful for, e.g. modulating
XX apoptosis and NF-KB activation and proinflammatory or autoimmune
XX responses.
XX
XX Example 2; Fig 5A; 104pp; English.
XX
XX The present sequence represents a putative ligand for PRO364 (see also
XX CC AAY06605), a novel member of the tumour necrosis factor receptor family.
XX The sequence was deduced from an isolated cDNA clone (see AAX87726).
XX CC Hydropathy analysis suggests a type II transmembrane homology. The
XX CC mol.wt. is 20,308. Identity is shown to human Apo-2L (19.8%), Fas/Apo1-
XX CC ligand (19.0%), TNF-alpha (20.6%) and lymphotoxin-alpha (17.5%). PRO364
XX is useful for modulating apoptosis, NF-KB activation and proinflammatory
XX or autoimmune responses in mammalian cells
XX
XX Sequence 177 AA:
SQ
Query Match 100.0%; Score 675; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.4e-69;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIAKEPCMAKFGPLPSKQWQASSEPPCVNKVSDMKLEILLONGLYLYGGVAPANANDVA 60
DB 52 EIAKEPCMAKFGPLPSKQWQASSEPPCVNKVSDMKLEILLONGLYLYGGVAPANANDVA 111
QY 61 PFEVRLYKKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIENSEHOVLKNNYTWGIIILA 120
DB 112 PFEVRLYKKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIENSEHOVLKNNYTWGIIILA 171
QY 121 NPOFIS 126
DB 172 NPOFIS 177
RESULT 8
AAB47056
XX AAB47056 standard; protein; 177 AA.
XX
XX AAB47056;
XX
XX 08-MAY-2001 (first entry)
XX
XX PRO175.
XX
XX PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
XX hGTR; ligand; hGTR; PRO175; tumour necrosis factor receptor; TNFR;
XX human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
XX myocardial infarction; PGF 2alpha; trauma; cancer; angiogenesis;
XX age-related macular degeneration; antibody; peridontal disease;
XX vasculature-related drug targeting; atherosclerosis; hypertension;
XX inflammatory vasculitis; Reynaud's disease; aneurysm;
XX arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
XX fibrosis; neuropathy; rheumatoid arthritis.
XX

```

OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Region 1..25 /note= "Cytoplasmic region"  
FT Region 26..51 /note= "Transmembrane region"  
FT Region 52..177 /note= "Extracellular region"  
FT Modified-site 129 /note= "N-glycosylated"  
FT Modified-site 161 /note= "N-glycosylated"  
FT Modified-site 161 /note= "N-glycosylated"  
XX WO200103720-A2.  
XX 18-JAN-2001.  
XX 11-JUL-2000; 2000WO-US018867.  
XX 12-JUL-1999; 99US-0143304P.  
XX (GETH ) GENENTECH INC.  
XX Williams PM, Gerritsen ME;  
XX WPI; 2001-138257/14.  
XX N-PSDB; AAC85435.  
XX Composition for diagnosing and treating cardiovascular, endothelial and  
XX angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.  
XX  
XX Claim 2; Fig 5; 76pp; English.

This sequence represents PRO175 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor ligand (hGITRL). The corresponding receptor (hGITR), PRO364, is given in AAB47054. PRO364 and PRO175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic agent for the treatment of a cardiovascular, endothelial, angiostatic or angiostatic disorder. The PRO364 sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was isolated from a library of cDNA fragments derived from human umbilical vein endothelial cells (HUVEC). Administering an effective amount of PRO364 or PRO175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGF 2alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering from a tumor or a retinal disorder. PRO364 or PRO175, or their antagonists, are useful for vascular-related drug targeting or as therapeutic targets for the treatment or prevention of atherosclerosis, hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms, arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal disease, attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis

Sequence 177 AA;

Query Match 100.0%; Score 675; DB 4; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2,4e-69;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETRAKPCMAKFGPLPSKQWMASSPPCVAKVSDMKLEIIQNGLYLIYGVANPNYNDVA 60  
DB 52 ETRAKPCMAKFGPLPSKQWMASSPPCVAKVSDMKLEIIQNGLYLIYGVANPNYNDVA 111  
QY 61 PEVEALYKXKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIINSEHQVLKNNYTWGIIILIA 120  
DB 112 PEVEALYKXKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIINSEHQVLKNNYTWGIIILIA 171

QY 121 NPOFIS 126  
DB 172 NPOFIS 177

RESULT 9  
AAB20109  
ID AAB20109 standard; protein; 177 AA.

XX AAB20109;  
XX 30-APR-2001 (first entry)  
XX

Human immunostimulant PRO175.

XX PRO175; UNQ149; human; immune disease; autoimmune disease; antirheumatic;  
XX antiarthritic; antiinflammatory; antianaemic; immunosuppressive;  
XX antihypertoid; antidiabetic; neuroprotective; hepatotropic; virucide;  
XX dermatological; antipsoriatic; antiasthmatic; antiallergic;  
XX immunostimulant.

XX Homo sapiens.

XX Key Location/Qualifiers  
XX Peptide 1..44 /label= Signal\_peptide  
XX Modified-site 18..24 /note= "N-myristoylation site"

XX Protein 45..177 /label= Mature\_protein  
XX Modified-site 129..133 /note= "Asn is N-glycosylated"  
XX Modified-site 161..165 /note= "Asn is N-glycosylated"

XX WO200105972-A1.

XX 25-JAN-2001.

XX 15-MAR-2000; 2000WO-US006884.

XX 20-JUL-1999; 99US-0144758P.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ,  
XX Gurney AL, Hillan KJ, Mark MK, Marsters SA, Pitti RM, Tumas D;  
XX Watanabe CK, Wood WI;  
XX WPI; 2001-103149/11.  
XX N-PSDB; AAF30051.

XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
XX diagnosis and treating immune-related disorders, such as multiple  
XX sclerosis, rheumatoid arthritis and diabetes.

XX Claim 20; Fig 4; 127pp; English.

XX The present sequence is that of PRO175 (UNQ149), a novel human  
XX immunomodulator protein (20 kDa, pI 8.08) showing homology to tumour  
XX necrosis factor family members. The invention provides polynucleotides  
XX (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)  
XX including PRO175. Claimed compositions comprising these proteins or their  
XX agonists are useful for increasing infiltration of inflammatory cells  
XX into a tissue of a mammal, stimulating or enhancing an immune response in  
XX a mammal, or increasing the proliferation of T-lymphocytes in a mammal in  
XX response to an antigen. Claimed compositions comprising the PRO  
XX polypeptide or its antagonist have the opposite effect. A claimed method  
XX for treating an immune related disorder, such as a T cell disorder,  
XX involves administering the PRO polypeptide, an agonist antibody or an  
XX antagonist antibody. The disorder is selected from systemic lupus  
XX erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic

CC arthritis, spondyloarthritis, systemic sclerosis, idiopathic  
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,  
 CC sarcoidosis, autoimmune hemolytic anaemia, autoimmune thrombocytopenia,  
 CC thyroditis, diabetes mellitus, immune-mediated renal disease,  
 CC demyelinated diseases (such as multiple sclerosis), autoimmune chronic  
 CC active hepatitis, primary biliary cirrhosis, granulomatous hepatitis,  
 CC sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis  
 CC and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease,  
 CC (auto) immune-mediated skin diseases (such as bullous skin disease,  
 CC erythema multiforme and psoriasis), allergic diseases (such as asthma,  
 CC urticaria), immunologic diseases of the lung and transplantation  
 CC associated diseases (such as graft rejection and graft-versus-host  
 CC disease) (all claimed). Claimed methods of diagnosing these disorders  
 CC comprise detecting the level of expression of the PRO gene. Also claimed  
 CC are a method of identifying a compound capable of inhibiting the  
 CC expression or activity of the PRO polypeptide, vectors, host cells,  
 CC antibodies, and a method of stimulating an immune response in a mammal  
 CC using PRO179  
 CC  
 SQ Sequence 177 AA;

Query Match 100.0%; Score 675; DB 4; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-69;  
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPPCAKFGPLPSKQMASSEPPCVNKSVDKLEILONGLYLYIGVAPNANVNDVA 60  
 DB 52 ETAKPPCAKFGPLPSKQMASSEPPCVNKSVDKLEILONGLYLYIGVAPNANVNDVA 111  
 QY 61 PFEVRLYNKMDMIQTITNSKIQNVGTYELHVGDTIDLFNSEHGVKNNYWGIIILA 120  
 DB 112 PFEVRLYNKMDMIQTITNSKIQNVGTYELHVGDTIDLFNSEHGVKNNYWGIIILA 171  
 QY 121 NPQFIS 126  
 DB 172 NPQFIS 177

RESULT 10  
 AAB53065  
 ID AAB53065 standard; protein; 177 AA.

AC AAB53065;  
 DT 28-FEB-2001 (first entry)  
 DE Human angiogenesis-associated protein PRO175, SEQ ID NO:9.  
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal.  
 OS Homo sapiens.  
 XX  
 XX WO200053753-A2.  
 XX  
 XX 14-SEP-2000.  
 PD  
 XX 05-JAN-2000; 2000WO-US000219.  
 PF  
 XX 08-MAR-1999; 99WO-US005028.  
 PR 12-MAR-1999; 99US-0123957P.  
 XX  
 PR 14-MAY-1999; 99US-0134287P.  
 XX  
 PR 02-JUN-1999; 99WO-US012252.  
 XX  
 PR 23-JUN-1999; 99US-0141037P.  
 XX  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 30-NOV-1999; 99WO-US028409.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Peoni NF, Plett RM, Watanabe CK, Williams PM, Wood WI;  
 DR WPI; 2001-090793/10.  
 DR N-PSDB; AAC97374.

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic  
 PT disorders, such as atherosclerosis, wounds or cancer.

PS Claim 69; Fig 4; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity; diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
 CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO  
 CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to screen  
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map  
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene  
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals  
 CC useful for the development and screening of potential therapeutic agents.  
 CC The present sequence represents a PRO protein of the invention  
 XX  
 SQ Sequence 177 AA;

Query Match 100.0%; Score 675; DB 4; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-69;  
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPPCAKFGPLPSKQMASSEPPCVNKSVDKLEILONGLYLYIGVAPNANVNDVA 60  
 DB 52 ETAKPPCAKFGPLPSKQMASSEPPCVNKSVDKLEILONGLYLYIGVAPNANVNDVA 111  
 QY 61 PFEVRLYNKMDMIQTITNSKIQNVGTYELHVGDTIDLFNSEHGVKNNYWGIIILA 120  
 DB 112 PFEVRLYNKMDMIQTITNSKIQNVGTYELHVGDTIDLFNSEHGVKNNYWGIIILA 171  
 QY 121 NPQFIS 126  
 DB 172 NPQFIS 177



02-MAR-2000; 2000OWO-US005841.  
 PR 10-MAR-2000; 2000OWO-US006319.  
 PR 15-MAR-2000; 2000OWO-US006884.  
 PR 21-MAR-2000; 2000OWO-US007532.  
 PR 30-MAR-2000; 2000OWO-US008439.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gertlesen ME;  
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX  
 WPI: 2001-025251/03.  
 DR N-PSDB; AAC90563.  
 XX  
 PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 PT disorders in a mammal.  
 XX  
 PS Claim 71, Fig 2, 182pp; English.  
 XX  
 CC The present sequence is one of seventeen novel PRO polypeptides. The PRO  
 CC nucleic acids, polypeptides, agonists and antagonists are useful for  
 CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
 CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
 CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
 CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
 CC antagonists are also used to prevent tumour angiogenesis and for treating  
 CC periodontal diseases. They are also used to stimulate wound healing and  
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder  
 XX  
 SQ Sequence 177 AA;  
 Query Match 100.0%; Score 675; DB 4; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-69;  
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETAKKPCMAKFGPLPSKQWMASSPPCVNKSVDWKLKLIQNGLYLYIGQVAPNANNVNDVA 60  
 Db 52 ETAKKPCMAKFGPLPSKQWMASSPPCVNKSVDWKLKLIQNGLYLYIGQVAPNANNVNDVA 111  
 QY 61 PEEVRLYKXKMDIQTLLNKSQKIQNVGTYELAHVDTIDILFNEHQVLLKNNYWGIIILA 120  
 Db 112 PEEVRLYKXKMDIQTLLNKSQKIQNVGTYELAHVDTIDILFNEHQVLLKNNYWGIIILA 171  
 QY 121 NPOFIS 126  
 Db 172 NPOFIS 177  
 Db  
 RESULT 13  
 AAU81953  
 ID AAU81953 standard; protein; 177 AA.  
 XX  
 AC AAU81953;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human PRO175.  
 XX  
 KW Human; PRO; antiinflammatory; ophthalmological; vasotropic;  
 KW retinal cell injury; ocular disease; retinitis pigmentosa;  
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
 KW retinal degenerative disease; macular hole; degenerative myopia;  
 KW acute retinal necrosis syndrome; traumatic chorioretinopathy;  
 KW Purtscher's retinopathy; oedema; ischaemic condition;  
 KW retinal vision occlusion; collagen vascular disease;  
 KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Bales disease;  
 KW systemic lupus erythematosus; environmental trauma.

OS Homo sapiens.  
 XX  
 PN WOJ00109327-A2.  
 XX  
 PD 08-FEB-2001.  
 XX  
 PF 28-JUL-2000; 2000OWO-US020710.  
 XX  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 05-JAN-2000; 2000OWO-US000219.  
 PR 06-JAN-2000; 2000OWO-US000376.  
 PR 11-FEB-2000; 2000OWO-US003565.  
 PR 18-FEB-2000; 2000OWO-US004341.  
 PR 22-FEB-2000; 2000OWO-US004414.  
 PR 24-FEB-2000; 2000OWO-US005004.  
 PR 02-MAR-2000; 2000OWO-US005841.  
 PR 15-MAR-2000; 2000OWO-US006884.  
 PR 30-MAR-2000; 2000OWO-US008439.  
 PR 17-MAY-2000; 2000OWO-US013705.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
 PI Ljavan J, Lafleur M, Mark MR, Marsters SA, Pitti RM, Watanabe CK;  
 PI Wood WI;  
 XX  
 WPI: 2002-130120/17.  
 DR N-PSDB; ABK28562.  
 XX  
 PT Promoting survival of retinal cells, or delaying or preventing retinal  
 PT cell injury or death, by contacting retinal cells with PRO175, 220, 216,  
 PT 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132 polypeptide.  
 XX  
 PS Claim 44; Fig 2; 152pp; English.  
 XX  
 CC The invention relates to promoting the survival of retinal cells, or  
 CC delaying or preventing retinal cell injury or death, by contacting the  
 CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
 CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO826, PRO826,  
 CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
 CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
 CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
 CC useful for promoting survival of retinal cells (retinal neurons such as  
 CC retinal ganglion cells, displaced retinal ganglion cells, amacrine cells,  
 CC photoreceptors, or supportive cells such as Muller cells or pigment  
 CC epithelial cells), or delaying or preventing retinal cell injury or death  
 CC caused by ocular disease (which is or is associated with retinitis  
 CC pigmentosa, macular degeneration, retinal detachment, retinal tear,  
 CC retinopathy, retinal degenerative disease, macular hole, degenerative  
 CC myopia, acute retinal necrosis syndrome, traumatic chorioretinopathy or  
 CC contusion, Purtscher's retinopathy, oedema, an ischaemic condition,  
 CC central or branch retinal vision occlusion, collagen vascular disease,  
 CC thrombocytopaenic purpura, uveitis, retinal vasculitis, occlusion  
 CC associated with Bales disease or systemic lupus erythematosus), retinal  
 CC injury or environmental trauma. The retinal cell injury or death is  
 CC delayed or prevented by substantially not causing angiogenesis or  
 CC mitogenesis. The present sequence represents a PRO protein  
 XX  
 SQ Sequence 177 AA;  
 Query Match 100.0%; Score 675; DB 5; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-69;  
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETAKKPCMAKFGPLPSKQWMASSPPCVNKSVDWKLKLIQNGLYLYIGQVAPNANNVNDVA 60  
 Db 52 ETAKKPCMAKFGPLPSKQWMASSPPCVNKSVDWKLKLIQNGLYLYIGQVAPNANNVNDVA 111

QY 61 PFEVRLYKKNKMDIQTLLTNKSKIONVGSTYELHVGDTIDLI.FNSEHGVYKKNNTYWGIIILLA 120  
| | | | |  
Db 112 PFEVRLYKKNKMDIQTLLTNKSKIONVGSTYELHVGDTIDLI.FNSEHGVYKKNNTYWGIIILLA 171  
QY 121 NPOFIS 126  
| | | | |  
Db 172 NPOFIS 177

RESULT 14  
ABR42323 standard; protein; 177 AA.  
ID ABR42323  
XX ABR42323;  
AC  
XX  
XX 11-AUG-2003 (first entry)  
DT  
XX Human GITRL protein.  
DB  
XX Human; GITRL; tumour necrosis factor; ligand; cytostatic;  
KW immunomodulator; osteopathic.  
KW  
XX Homo sapiens.  
OS  
XX WO2003040307-A2.  
PN  
XX 15-MAY-2003.  
PD  
XX 25-JUL-2002; 2002WO-US023782.  
PE  
XX 27-JUL-2001; 2001US-0307838P.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Hilbert DE, Rosen CA;  
PI  
XX WPI; 2003-430659/40.  
DR N-PSDB; ACC57909.  
DR  
XX New heteromultimeric complex having a first polypeptide member of the  
PT tumor necrosis factor (TNF) ligand family, and a second different member  
PT of TNF ligand family, useful for treating cancer, osteoporosis or an  
PT autoimmune disease.  
PT  
XX Disclosure; Page 382-383; 388pp; English.

PS The present sequence is the protein sequence of human GITRL polypeptide.  
XX The invention relates to compositions comprising heterotrimeric complexes  
CC of tumour necrosis factor (TNF) ligand family members, and their use in  
CC the detection, prevention and treatment of disease. In preferred  
CC embodiments, the heterotrimeric complex comprises full-length or  
CC extracellular portions of GITRL together with full-length or  
CC extracellular portions of other TNF ligand family members. The  
CC heterotrimeric complexes of the invention are useful for treating an  
CC autoimmune disease, cancer or osteoporosis, and particularly for  
CC inhibiting cancer cell proliferation, increasing B cell proliferation, or  
CC inducing apoptosis of T cells  
CC  
XX Sequence 177 AA;

Query Match 100.0%; Score 675; DB 6; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2.4e-69;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETRAKEPCMAKFGP.LPSKQWMASSPPCVNKKVSDMKLEII.QNGILYLYGVVAPNANYNDVA 60  
| | | | |  
Db 52 ETRAKEPCMAKFGP.LPSKQWMASSPPCVNKKVSDMKLEII.QNGILYLYGVVAPNANYNDVA 111  
QY 61 PFEVRLYKKNKMDIQTLLTNKSKIONVGSTYELHVGDTIDLI.FNSEHGVYKKNNTYWGIIILLA 120  
| | | | |  
Db 112 PFEVRLYKKNKMDIQTLLTNKSKIONVGSTYELHVGDTIDLI.FNSEHGVYKKNNTYWGIIILLA 171

QY 121 NPOFIS 126  
| | | | |  
Db 172 NPOFIS 177

RESULT 15  
ABP60544 standard; protein; 177 AA.  
ID ABP60544  
XX ABP60544;  
AC  
XX 28-MAR-2003 (first entry)  
DT  
XX Human tumour necrosis factor endokine-alpha.  
DE  
XX APRIL; gcfv; immunospecific; tumour necrosis factor delta; TNF-delta;  
KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;  
KW antiarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic;  
KW neuroprotective; ophthalmological; tuberculosstatic; antidiabetic;  
KW antiporiatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;  
KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;  
KW inflammatory disorder; proliferative disorder; single chain antibody;  
KW antibody; human; tumour necrosis factor; endokine-alpha.  
KW  
XX Homo sapiens.  
OS  
XX WO200294192-A2.  
PN  
XX 28-NOV-2002.  
PD  
XX 22-MAY-2002; 2002WO-US016106.  
PE  
XX 24-MAY-2001; 2001US-0293100P.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Ruben SM;  
PI  
XX WPI; 2003-156740/15.  
DR  
XX Novel isolated antibody that immunospecifically binds tumor necrosis  
PT factor delta, useful for treating, preventing or ameliorating Non-  
PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's  
PT syndrome.  
PT  
XX Disclosure; Page 214-215; 225pp; English.

PS The invention relates to a novel antibody or its fragment, which  
XX immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).  
CC The antibody of the invention has dermatological, immunosuppressive,  
CC antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,  
CC antiallergic, antiasthmatic, neuroprotective, ophthalmological,  
CC tuberculosstatic, antidiabetic, antiporiatic, anti-HIV,  
CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.  
CC The antibody or its fragment are useful for treating, preventing or  
CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in  
CC human, disease or disorder such as autoimmune disease, and graft versus  
CC host disease (GVHD). The autoimmune disease is systemic lupus  
CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody  
CC is useful for detecting, diagnosing, prognosing, treating, preventing or  
CC ameliorating a disease or disorder associated with aberrant APRIL or  
CC APRIL receptor expression or aberrant function of APRIL or APRIL  
CC receptor. The disease or disorders includes autoimmune and inflammatory  
CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,  
CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,  
CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune  
CC system, particularly B cell cancers, immune disorders such as myasthenia  
CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,  
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and  
CC proliferative disorders (e.g. leukemia). The present sequence represents  
CC the tumour necrosis factor endokine-alpha  
XX  
XX Sequence 177 AA;



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 2, 2004, 12:50:37 ; Search time 39 Seconds  
(without alignments)  
214.258 Million cell updates/sec

Title: US-10-080-455-1\_COPY\_52\_177

Perfect score: 675  
Sequence: 1 ETRKEPCMAKFGPLPSKWMQ.....VLKNNTYGIILLNPQFIS 126

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pep: \*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pep: \*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep: \*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep: \*  
5: /cgn2\_6/prodata/1/iaa/PCtUS COMB.pep: \*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	675	100.0	169	2	US-08-912-227-2
2	675	100.0	169	4	US-09-513-584-2
3	675	100.0	169	4	US-09-345-790-2
4	84.5	12.5	1221	4	US-09-107-532A-3959
5	77	11.4	217	4	US-09-248-796A-20671
6	76	11.3	2763	3	US-08-496-944-2
7	74	11.0	157	5	PCT-US93-02475-6
8	74	11.0	235	4	US-09-270-767-49088
9	74	11.0	543	3	US-08-697-610-2
10	74	11.0	543	3	US-08-349-357-2
11	74	11.0	567	4	US-09-645-926A-7
12	73	10.8	289	4	US-09-248-796A-15058
13	72	10.7	609	4	US-09-396-149-6
14	71	10.5	157	5	PCT-US93-02475-2
15	71	10.5	620	4	US-09-710-879-606
16	71	10.5	621	4	US-09-710-879-2614
17	71	10.5	680	4	US-09-583-110-3191
18	70.5	10.4	396	4	US-09-248-796A-19923
19	70	10.4	157	5	PCT-US93-02475-7
20	70	10.4	641	4	US-09-248-796A-17974
21	69.5	10.3	211	4	US-09-322-409-78
22	69.5	10.3	211	4	US-09-451-527-78
23	69.5	10.3	235	4	US-09-131-237C-7
24	69.5	10.3	260	4	US-09-322-409-73
25	69.5	10.3	260	4	US-09-451-527-73
26	69.5	10.3	422	4	US-09-270-767-42572
27	69.5	10.3	964	1	US-08-257-073-3

28	69.5	10.3	984	2	US-08-184-009-120	Sequence 120, App
29	69.5	10.3	984	2	US-08-458-356-120	Sequence 120, App
30	69.5	10.3	984	3	US-08-460-736-120	Sequence 120, App
31	69.5	10.3	984	4	US-09-535-370-120	Sequence 120, App
32	69.5	10.3	984	4	US-09-663-667-120	Sequence 120, App
33	69.5	10.3	984	3	US-08-213-419B-2	Sequence 2, App1
34	69.5	10.3	984	3	US-08-213-419B-4	Sequence 4, App1
35	69.5	10.3	1013	4	US-09-255-829-18	Sequence 18, App1
36	69	10.2	634	4	US-09-543-681A-7019	Sequence 7019, App
37	68.5	10.1	1604	3	US-09-004-838-95	Sequence 95, App1
38	68.5	10.1	3443	2	US-08-416-603-2	Sequence 2, App1
39	68.5	10.1	3623	4	US-09-341-461-2	Sequence 16516, A
40	68	10.1	487	4	US-09-248-796A-16516	Sequence 70, App1
41	67.5	10.0	211	4	US-09-322-409-70	Sequence 70, App1
42	67.5	10.0	211	4	US-09-451-527-70	Sequence 70, App1
43	67.5	10.0	260	4	US-09-322-409-65	Sequence 65, App1
44	67.5	10.0	260	4	US-09-451-527-65	Sequence 65, App1
45	67.5	10.0	289	4	US-09-589-287B-38	Sequence 38, App1

## ALIGNMENTS

RESULT 1  
US-08-912-227-2  
Sequence 2, Application US/08912227  
Patent No. 5998171  
GENERAL INFORMATION:  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ni, Jian  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: Human Endokine Alpha  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,227  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/024,058  
FILING DATE: 16-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0470001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 169 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-912-227-2

Query Match 100.0%; Score 675; DB 2; Length 169;  
Best local similarity 100.0%; Pred. No. 2, 2e-75;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 ETRKEPCMAKFGPLPSKWMASSEPCNKVSDWKLEIIQNGLYLTYGVAPNANYNDVA 60  
|||||

Db 44 ETKAPECKAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 103  
QY 61 PFEVRLYKXKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 120  
Db 104 PFEVRLYKXKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 163  
QY 121 NPQFIS 126  
Db 164 NPQFIS 169

## RESULT 2

US-09-513-584-2  
; Sequence 2, Application US/09513584  
; Patent No. 6406867  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Human Endokline Alpha and Methods  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX,  
; ADDRESS: P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/513,584  
; FILING DATE: 25-FEB-2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,058  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,227  
; FILING DATE: 15-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/122,099  
; FILING DATE: 26-FEB-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/136,788  
; FILING DATE: 28-MAY-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/345,790  
; FILING DATE: 01-JUL-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0470005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-513-584-2

Query Match 100.0%; Score 675; DB 4; Length 169;  
Best Local Similarity 100.0%; Pred. No. 2.2e-75;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKAPECKAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 60  
Db 44 ETKAPECKAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 103  
QY 61 PFEVRLYKXKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 120  
Db 104 PFEVRLYKXKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 163  
QY 121 NPQFIS 126  
Db 164 NPQFIS 169

## RESULT 3

US-09-345-790-2  
; Sequence 2, Application US/09345790  
; Patent No. 6521742  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Human Endokline Alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/345,790  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/912,227  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0470001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-345-790-2

Query Match 100.0%; Score 675; DB 4; Length 169;  
Best Local Similarity 100.0%; Pred. No. 2.2e-75;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKAPECKAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 60  
Db 44 ETKAPECKAKFGPLPSKQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDVA 103  
QY 61 PFEVRLYKXKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 120  
Db 104 PFEVRLYKXKMDIQTITNKSXIQNVGTYELHVGDTIDLIINSEHOVLKNNYWGIIILA 163  
QY 121 NPQFIS 126  
Db 164 NPQFIS 169

```

US-09-107-532A-3959
; Sequence 3959, Application US/09107532A
; Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 3959:
SEQUENCE CHARACTERISTICS:
LENGTH: 1221 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1221
SEQUENCE DESCRIPTION: SEQ ID NO: 3959:
US-09-107-532A-3959

Query Match      12.5%; Score 84.5; DB 4; Length 1221;
Best Local Similarity 28.8%; Pred. No. 0.45;
Matches 19; Conservative 19; Mismatches 23; Indels 5; Gaps 1;

QY   51  APNANYNVAAPEVEVLYNKDMIOFLTNKS-----KIQNGGTYELHGDITDLTFNESEH 105
     ||| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    515  APNGQDSSRSFTVKENONVTTRINKSGSVIEIKIGDGLGLPNNVFPTTYSNDN 574
     : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   106  QVLKNR 111
     : : : : :
Db    575  KVVKDQ 580

RESULT 5
US-09-248-796A-20671
; Sequence 20671, Application US/09248796A
; Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FOR DIAGNOSTICS AND THERAPEUTICS
```

```

FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20671
LENGTH: 217
TYPE: PRF
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (15)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are
US-09-248-796A-20671

Query Match
Best Local Similarity 11.4%; Score 77; DB 4; Length 217;
Matches 31; Conservative 13; Mismatches 44; Indels 26; Gaps 7;

CY 15 PSKMQMASS--EPP-----CVNKYSDWKLFTLQGLYLYGQVAP---NNYNDVAPF 62
DB 85 PDMWDAAKQWEPPLIVNPKCATGGCPWEPALPIPHNDYI--GPMPPPDIKENYNGI--W 140
CY 63 EVRLYKKNOMIQTLTNKSQIQNVGT-YELHVGDTIDLIENSEHOVLKNNTYWG 115
DB 141 TPRLIPNDYVQVKTPGKLDKPIGIGFEL-----WSIESILFDNIYIYG 185

RESULT 6
US-08-496-944-2
Sequence 2, Application US/08496944
Patent No. 6040496
GENERAL INFORMATION:
APPLICANT: Law, Marcus D
APPLICANT: Dietz, Jon M
TITLE OF INVENTION: Use of translationally altered RNA to
TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other
TITLE OF INVENTION: Monocotyledonous Plant Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,944
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1814
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-496-944-2

Query Match
Best Local Similarity 11.3%; Score 76; DB 3; Length 2763;
Matches 31; Conservative 18; Mismatches 51; Indels 20; Gaps 5;

```

QY 4 KEEPMAGFGLPSKQWASSEPPCVNKVSPDKLEILLQNGHYLYIGQVAPNANYNDVAFPE 63  
DB 22 KERCNPEFESHLPTLMQVAFETIGHYTDNOSQIMDV-SEALIKVTLPPDDAMKASALLLE 80  
QY 64 V-RLYRKNK-----DMIQTLTKNSKIONVGCTEYELHVGDTITDLIFNSEHGYLKR-KTYNG 115  
DB 81 VSRWYKNRKESLKTDLSEFRNK-----ISPKSTINAMCMQDLDKKNANFVWG 129

RESULT 7  
PCT-US93-02475-6  
Sequence 6, Application PC/TUS9302475  
GENERAL INFORMATION:  
APPLICANT: Winiieski, Bernadine J.  
TITLE OF INVENTION: Tumor Necrosis Factor with Modified  
TITLE OF INVENTION: Ion Channel  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Donald G. Lewis  
STREET: 8328 Regents Road #1E  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage  
COMPUTER: VE System 386  
OPERATING SYSTEM: MS-DOS 5  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02475  
FILING DATE: 19930412  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/852,625  
FILING DATE: 12 March 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Donald G. Lewis  
REGISTRATION NUMBER: 28636  
REFERENCE/DOCKET NUMBER: BJW-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2421  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: AMINO ACIDS  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Tumor Necrosis Factor (feline)  
PUBLICATION INFORMATION:  
AUTHORS: McGraw, R. A., Coffee, B. W., Otto,  
AUTHORS: C. M., Drews, R. T. and Rawling, C. A.  
TITLE: Gene Sequence of Feline Tumor Necrosis  
TITLE: Factor  
JOURNAL: Nucleic Acids Research  
VOLUME: 18  
PAGES: 5564  
DATE: 1990  
RELEVANT RESIDUES IN SEQ ID NO: 6: 1-157  
PCT-US93-02475-6

Query Match 11.0%; Score 74; DB 5; Length 157;  
Best Local Similarity 24.4%; Pred. No. 0.45;  
Matches 30; Conservative 21; Mismatches 32; Indels 40; Gaps 6;  
QY 30 KVDWKLEILLQNGHYLYIGQV-----APNANY-----NDVAPPEVRLYKKNKDMIQTLTKNS 80  
DB 42 ELTDQKLKVPDGLYLYISQVLFYGGGCSSTHVLTLHAISRFAVSQYQTVKNLISAL--KS 99  
QY 81 KIQN-----VGCTEYELHVGDTITD-----LIFNSEHGYLKNNTYWG 116

DB 100 PCQREPEGAERAKWPYPIYIGVFOLEKDRRLSTEINLPAYIDFASQGV-----YFGI 154  
QY 117 ILL 119  
DB 155 IAL 157

RESULT 8  
US-09-270-767-49088  
Sequence 49088, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 49088  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-49088

Query Match 11.0%; Score 74; DB 4; Length 235;  
Best Local Similarity 32.4%; Pred. No. 0.81; 31; Indels 28; Gaps 7;  
Matches 33; Conservative 10; Mismatches 28; Indels 28; Gaps 7;

QY 35 KLEILLQNGHYLYIGQV-APNANY-NDV-----APFEVRLYKKNKDMIQTLTKN 79  
DB 20 KLEPLKE-IMKIKQVSSARANRFRDIPQVHARHAMQAEYERQSKAE-----TKT 73  
QY 80 SKIQNVGTY-----ELHVGDT-IDLIFNSEHGYLKNNTY 114  
DB 74 KEFQYNGKYALEQSHLIIDTPTVTLFNRDHSVLLITW 115

RESULT 9  
US-08-697-610-2  
Sequence 2, Application US/08697610  
Patent No. 6172187  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaaki  
TITLE OF INVENTION: CD40 Associated Proteins  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/697,610  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/349,357  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-1J 1203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 543 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-697-610-2

Query Match 11.0%; Score 74; DB 3; Length 543;  
Best Local Similarity 28.3%; Pred. No. 2.7;  
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 21 ASSEPPCVNKSVDW-----KLEILONGLYLYGQVAPNAN---YNDVAPFEVRLYK 70  
DB 228 ASSAVGVHVLKEMSNLSLEKVSILQN-----ESVEKNKSIGSLNHQICSFEIEROK 281

QY 71 DMIQTLNKSQIONVGGTYELHVGDTIDLIENSEHQVLK 109  
DB 282 EMLR--NNESKI-----LHLQRYID---SQAEKTK 306

## RESULT 10

US-08-349-357-2  
Sequence 2, Application US/08349357  
Patent No. 6265556  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaaki  
TITLE OF INVENTION: CD40 Associated Proteins  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/349,357  
FILING DATE: 02-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 543 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-349-357-2

Query Match 11.0%; Score 74; DB 3; Length 543;  
Best Local Similarity 28.3%; Pred. No. 2.7;  
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 21 ASSEPPCVNKSVDW-----KLEILONGLYLYGQVAPNAN---YNDVAPFEVRLYK 70  
DB 228 ASSAVGVHVLKEMSNLSLEKVSILQN-----ESVEKNKSIGSLNHQICSFEIEROK 281

QY 71 DMIQTLNKSQIONVGGTYELHVGDTIDLIENSEHQVLK 109  
DB 282 EMLR--NNESKI-----LHLQRYID---SQAEKTK 306

## RESULT 11

US-09-645-926A-7  
Sequence 7, Application US/09645926A  
Patent No. 6482411  
GENERAL INFORMATION:  
APPLICANT: AHUJA, SEEMA  
APPLICANT: BONEWALD, LYNDIA  
TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE  
FILE REFERENCE: 4003.001000  
CURRENT APPLICATION NUMBER: US/09/645,926A  
CURRENT FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: 60/151,250  
PRIOR FILING DATE: 1999-08-27  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 7  
LENGTH: 567  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-645-926A-7

Query Match 11.0%; Score 74; DB 4; Length 567;  
Best Local Similarity 28.3%; Pred. No. 2.9;  
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 21 ASSEPPCVNKSVDW-----KLEILONGLYLYGQVAPNAN---YNDVAPFEVRLYK 70  
DB 252 ASSAVGVHVLKEMSNLSLEKVSILQN-----ESVEKNKSIGSLNHQICSFEIEROK 305

QY 71 DMIQTLNKSQIONVGGTYELHVGDTIDLIENSEHQVLK 109  
DB 306 EMLR--NNESKI-----LHLQRYID---SQAEKTK 330

## RESULT 12

US-09-248-796A-15058  
Sequence 15058, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:  
APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 15058  
LENGTH: 289  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-15058

Query Match 10.8%; Score 73; DB 4; Length 289;  
Best Local Similarity 22.7%; Pred. No. 1.4;  
Matches 30; Conservative 23; Mismatches 37; Indels 42; Gaps 6;

QY 20 MASSEPPCVNKSVDWLEILIQ--NGLYLYGQVAPNANVNDVAPFEVRLY-----KN 69  
DB 143 IAINKSSISLADLKYQVYFYFNGIY-----NPISSYVRLPKFSIPKYGTSSEVNP 196

QY 70 KMIQTLNKSQ--IQNV-----GGTYELHVGDTIDLIENSEHQVLK 113  
DB 197 KRSIHITLNNYKFFQVNIETADKYHMLTIRANTKRIQYIYKLFYNSB-----247

QY 114 WGIILLANPQFI 125  
DB 248 -GILLRNDIFM 258

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RESULT 13
US-09-396-149-6
; Sequence 6, Application US/09396149
; Patent No. 6538176
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; TITLE OF INVENTION: Maize Replication Protein A and Use
; FILE REFERENCE: 5718-59
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-396-149-6

Query Match          10.7%; Score 72; DB 4; Length 609;
Best Local Similarity 24.3%; Pred. No. 5.7;
Matches 36; Conservative 25; Mismatches 51; Indels 36; Gaps 9;

QY 3 AKPCMAKFGPLSPKQMASSPPCVNKVSDMKLEILLNGLYLYIGQVA---PYANYND 58
DB 127 AAPAPASAP-AAPAPSKLQNNASAPPSPMNR-----GTSKLPFGGSLNTPGSGSOK 174
QY 59 VAPF-EVRLYKXKMDIQT-LTNKSKIQ--NVGTYELHVGDTID-----LIFNSEHQ 106
DB 175 VVPLASLNPYOSKMTVARAVTKGQIRFTWSNRSRGSKLFSIEMVDSGEIRATAFNEQAD 234
QY 107 -----VLKNTYV--GIILLANPOFIS 126
DB 235 KFFSIIEVXKYVFSKGTLLKLANKQYTS 262

RESULT 14
PCT-US93-02475-2
; Sequence 2, Application PC/TUS9302475
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Bernadine J.
; TITLE OF INVENTION: Tumor Necrosis Factor with Modified
; TITLE OF INVENTION: Ion Channel
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Donald G. Lewis
; STREET: 8328 Regents Road #1E
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage
; COMPUTER: VE System 386
; OPERATING SYSTEM: MS-DOS 5
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02475
; FILING DATE: 19930412
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,625
; FILING DATE: 12 March 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Donald G. Lewis
; REGISTRATION NUMBER: 28636
; REFERENCE/DOCKET NUMBER: BUW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2421
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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```
LENGTH: 157 amino acids
TYPE: AMINO ACIDS
TOPOLOGY: Linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Tumor Necrosis Factor (porcine)
OTHER INFORMATION: A blank residue designated by
OTHER INFORMATION: "xaa" is inserted after residue No. 7 of porcine
OTHER INFORMATION: TNF and the sequence numbering is augmented by 1
OTHER INFORMATION: starting with residue No. 8 in order to maximize
PUBLICATION INFORMATION:
AUTHORS: Pauli, U., Beutler, B., and Peterhans, S.
TITLE: Porcine Tumor Necrosis Factor--Cloning with
TITLE: the Polymerase Chain Reaction and Determination of
JOURNAL: Gene
VOLUME: 81
PAGES: 185-191
DATE: 1989
RELEVANT RESIDUES IN SEQ ID NO: 2: 1-157 (includes
RELEVANT RESIDUES IN SEQ ID NO: one blank)
PCT-US93-02475-2

Query Match          10.5%; Score 71; DB 5; Length 157;
Best Local Similarity 23.9%; Pred. No. 1;
Matches 33; Conservative 19; Mismatches 44; Indels 42; Gaps 7;

QY 17 KWQASSEPPCVN--KVSMDKLEILLNGLYLYIGQV-----APVANY--NDVAPFEVR 65
DB 27 QMOGYANALLANGVKLEKMDQVLPDGLYLYSQVLEFRGGCGSTVNFELTHTSRLAVS 86
QY 66 LYXKMDIQT-LTNKSKIQN-----VGGTYELHVGDTID-----LIF 101
DB 87 YQTKVNLISAI--KSPCQRETPEGAEKAWYEPYLGAVFQLEKDDRLSALINLPDYIDF 144
QY 102 NSEHQVLKNTYWGIIIL 119
DB 145 AESQGV-----YFGIIL 157

RESULT 15
US-09-710-279-606
; Sequence 606, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US/09/710,279
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 606
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-606

Query Match          10.5%; Score 71; DB 4; Length 620;
Best Local Similarity 23.0%; Pred. No. 7.8;
Matches 26; Conservative 20; Mismatches 33; Indels 34; Gaps 4;

QY 16 SKWQASSEPPCVNKVSDMKLEILLNGLYLYIGQVAPNANYDVAPFEVRLYKXKMDIQT 75
DB 450 NEWORI-----MMSQGRFVVLNANGFVELYGYTTINVDK-----DVTVGINRIVQN 495
QY 76 L-----TNKSKIQNVGTYELHVGDTIDLLIFNSEHQVLKNTYWGIIILANPQ 123
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Tue Nov 2 13:51:41 2004

us-10-080-455-1\_copy\_52\_177.raii

Page 7

Db  
496 YHPFEGFNKSRKRN-----LFSIEHRLNKGTTFPIYAAGVQ 533

Search completed: November 2, 2004, 13:00:14  
Job time : 40 secs

is Page Blank (uspto)



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2004, 12:58:53 : Search time 126 Seconds  
(without alignments)  
324.216 Million cell updates/sec

Title: US-10-080-455-1\_COPY\_52\_177

Perfect score: 675  
Sequence: 1 ETKRCPMAKFGPLPSKMQM.....VLKNNTYWGIIILANPQFIS 126

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: Published Applications\_AA:\*  
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19: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	169	9	US-09-345-790-2
2	675	100.0	169	13	US-10-136-511-2
3	675	100.0	177	13	US-10-080-455-1
4	675	100.0	177	13	US-10-116-378-16
5	675	100.0	177	14	US-10-151-882-39
6	675	100.0	177	14	US-10-218-547-40
7	675	100.0	177	14	US-10-310-793-44
8	675	100.0	177	15	US-10-202-062-40
9	608	90.1	113	14	US-10-338-083-17
10	608	90.1	113	16	US-10-611-399-17
11	75.5	11.2	5795	9	US-09-815-242-12610
12	74	11.0	543	9	US-09-757-041-2
13	74	11.0	543	14	US-10-004-378A-35

14	74	11.0	566	8	US-08-813-323A-1	Sequence 1, Appl1
15	74	11.0	567	14	US-10-242-212-7	Sequence 7, Appl1
16	74	11.0	567	14	US-10-207-655-103	Sequence 103, App
17	74	11.0	568	8	US-08-813-323A-2	Sequence 2, Appl1
18	74	11.0	568	14	US-10-116-275-173	Sequence 173, App
19	74	11.0	568	14	US-10-004-378A-36	Sequence 36, Appl
20	74	11.0	568	15	US-10-432-865-166	Sequence 166, App
21	74	11.0	819	16	US-10-437-963-184313	Sequence 184313,
22	73.5	10.9	1419	16	US-10-437-963-125464	Sequence 125464,
23	73	10.8	313	15	US-10-424-599-231929	Sequence 231929,
24	73	10.8	514	14	US-10-295-074-49	Sequence 49, Appl
25	73	10.8	514	14	US-10-295-074-51	Sequence 51, Appl
26	73	10.8	514	14	US-10-295-074-59	Sequence 59, Appl
27	73	10.8	517	14	US-10-295-074-53	Sequence 53, Appl
28	72	10.7	601	15	US-10-424-599-209463	Sequence 209463,
29	72	10.7	609	14	US-10-372-686-6	Sequence 6, Appl1
30	72	10.7	609	14	US-10-371-558-6	Sequence 6, Appl1
31	72	10.7	609	14	US-10-375-553-6	Sequence 6, Appl1
32	72	10.7	609	15	US-10-372-553-6	Sequence 6, Appl1
33	72	10.7	624	16	US-10-437-963-153543	Sequence 153543,
34	71.5	10.6	252	14	US-10-154-759-16	Sequence 16, Appl
35	71.5	10.6	252	14	US-10-154-759-18	Sequence 18, Appl
36	71.5	10.6	260	14	US-10-154-759-15	Sequence 15, Appl
37	71.5	10.6	260	14	US-10-154-759-17	Sequence 17, Appl
38	71.5	10.6	377	14	US-10-295-027-280	Sequence 280, App
39	71	10.5	157	14	US-10-295-074-42	Sequence 42, Appl
40	71	10.5	290	15	US-10-282-122A-71355	Sequence 71355, A
41	71	10.5	685	9	US-09-815-242-13477	Sequence 13477, A
42	71	10.5	685	15	US-10-282-122A-74118	Sequence 74118, A
43	71	10.5	685	16	US-10-474-776-710	Sequence 710, App
44	70.5	10.4	724	16	US-10-437-963-159310	Sequence 159310,
45	70	10.4	158	14	US-10-297-942-2	Sequence 2, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-345-790-2  
; Sequence 2, Application US/09345790  
; Patent No. US2002009198A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jjian  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Human Endokine Alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/345,790  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/912,227  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0470001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 169 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-345-790-2

Query Match 100.0%; Score 675; DB 9; Length 169;  
Best Local Similarity 100.0%; Pred. No. 3,1e-67;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDVA 60  
DB 44 EFAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDVA 103  
QY 61 PPEVLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 120  
DB 104 PPEVLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 163  
QY 121 NPOFIS 126  
DB 164 NPOFIS 169

#### RESULT 2

US-10-136-511-2  
Sequence 2, Application US/10136511  
Publication No. US20020168729A1  
GENERAL INFORMATION:  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ni, Jian  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: Human Endokine Alpha and Methods of Use  
FILE REFERENCE: 1468.0470007/EKS/PSC  
CURRENT FILING DATE: 2002-05-02  
PRIOR FILING DATE: 2000-02-25  
PRIOR APPLICATION NUMBER: 09/513,584  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: 09/345,790  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: 60/136,788  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/122,099  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 08/912,227  
PRIOR FILING DATE: 1997-08-15  
PRIOR APPLICATION NUMBER: 60/024,058  
PRIOR FILING DATE: 1996-08-16  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 169  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-136-511-2

Query Match 100.0%; Score 675; DB 13; Length 169;  
Best Local Similarity 100.0%; Pred. No. 3,1e-67;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDVA 60  
DB 44 EFAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDVA 103  
QY 61 PPEVLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 120  
DB 104 PPEVLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 163  
QY 121 NPOFIS 126  
DB 164 NPOFIS 169

#### RESULT 3

US-10-080-455-1  
Sequence 1, Application US/10080455  
Publication No. US20020146389A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Mark, Melanie R.  
APPLICANT: Maresfers, Scott A.  
APPLICANT: Pitti, Robert M.  
TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog  
FILE REFERENCE: P1150R2  
CURRENT APPLICATION NUMBER: US/10/080,455  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 09/195,368  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: US 60/069,661  
PRIOR FILING DATE: 1997-12-12  
PRIOR APPLICATION NUMBER: US 60/065,635  
PRIOR FILING DATE: 1997-11-18  
NUMBER OF SEQ ID NOS: 8  
SEQ ID NO 1  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-080-455-1

Query Match 100.0%; Score 675; DB 13; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3,3e-67;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 52 EFAKPPCAKFGPLPSKQMASSEPPCVKVDWKLEILQNGLYLYIGVAPNANYNDVA 111  
QY 61 PPEVLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 120  
DB 112 PPEVLYNKKDMIQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIILA 171  
QY 121 NPOFIS 126  
DB 172 NPOFIS 177

#### RESULT 4

US-10-116-378-16  
Sequence 16, Application US/10116378  
Publication No. US20020150993A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin  
APPLICANT: Maresfers, Scott A.  
APPLICANT: Pitti, Robert M.  
APPLICANT: Wood, William  
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND  
TITLE OF INVENTION: NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P1206R1  
CURRENT APPLICATION NUMBER: US/10/116,378  
CURRENT FILING DATE: 2002-04-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09  
NUMBER OF SEQ ID NOS: 31  
SEQ ID NO 16  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo sapiens



Db 52 ETAKPCKAKGFLPSKQWASSPCCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVA 111  
QY 61 PFEVRLYKXKMDIQTLLNKSXKIQNVGTYELHVGDTIDLLFNSEHQLKNNTYGIIILA 120  
Db 112 PFEVRLYKXKMDIQTLLNKSXKIQNVGTYELHVGDTIDLLFNSEHQLKNNTYGIIILA 171  
QY 121 NPQFIS 126  
Db 172 NPQFIS 177

RESULT 8  
US-10-202-062-40  
; Sequence 40, Application US/10202062  
; Publication No. US20040038349A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.,  
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members  
; FILE REFERENCE: PF559  
; CURRENT APPLICATION NUMBER: US/10/202,062  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,838  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 40  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: human  
US-10-202-062-40

Query Match 100.0%; Score 675; DB 15; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.3e-67;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 112 PFEVRLYKXKMDIQTLLNKSXKIQNVGTYELHVGDTIDLLFNSEHQLKNNTYGIIILA 171  
QY 121 NPQFIS 126  
Db 172 NPQFIS 177

RESULT 9  
US-10-338-083-17  
; Sequence 17, Application US/10338083  
; Publication No. US2003016559A1  
; GENERAL INFORMATION:  
; APPLICANT: Desjardais, John R.  
; APPLICANT: Tansey, Malu Lourdes G.  
; APPLICANT: Dahiyat, Basil I.  
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof  
; FILE REFERENCE: A-71273-2  
; CURRENT APPLICATION NUMBER: US/10/338,083  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/345,805  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: US 60/373,453  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-338-083-17  
Query Match 90.1%; Score 608; DB 14; Length 113;

Best Local Similarity 100.0%; Pred. No. 5.7e-60;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 CMAKFGPLPSKQWASSPCCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVAFPEVRL 60  
QY 67 YKXKMDIQTLLNKSXKIQNVGTYELHVGDTIDLLFNSEHQLKNNTYGIIILA 119  
Db 61 YKXKMDIQTLLNKSXKIQNVGTYELHVGDTIDLLFNSEHQLKNNTYGIIILA 113

RESULT 10  
US-10-611-399-17  
; Sequence 17, Application US/10611399  
; Publication No. US20040170602A1  
; GENERAL INFORMATION:  
; APPLICANT: Desjardais, John R.  
; APPLICANT: Tansey, Malu Lourdes G.  
; APPLICANT: Dahiyat, Basil I.  
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF  
; FILE REFERENCE: A-71273-3  
; CURRENT APPLICATION NUMBER: US/10/611,399  
; CURRENT FILING DATE: 2003-07-01  
; PRIOR APPLICATION NUMBER: US 10/338,083  
; PRIOR FILING DATE: 2003-01-06  
; PRIOR APPLICATION NUMBER: US 60/345,805  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: US 60/373,453  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-611-399-17

Query Match 90.1%; Score 608; DB 16; Length 113;  
Best Local Similarity 100.0%; Pred. No. 5.7e-60;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CMAKFGPLPSKQWASSPCCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVAFPEVRL 66  
Db 1 CMAKFGPLPSKQWASSPCCVNVKSDMKLEILLQNGLYLIYGQVAPNANYNDVAFPEVRL 60  
QY 67 YKXKMDIQTLLNKSXKIQNVGTYELHVGDTIDLLFNSEHQLKNNTYGIIILA 119  
Db 61 YKXKMDIQTLLNKSXKIQNVGTYELHVGDTIDLLFNSEHQLKNNTYGIIILA 113

RESULT 11  
US-09-815-242-12610  
; Sequence 12610, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: fastseq for windows version 4.0  
SEQ ID NO 12610  
LENGTH: 5795  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-09-815-242-12610

Query Match 11.2%; Score 75.5; DB 9; Length 5795;  
Best Local Similarity 27.4%; Pred. No. 3.5e+02;  
Matches 31; Conservative 17; Mismatches 40; Indels 25; Gaps 6;

QY 14 LPSKMQASSEPCVKNVSKWLEILONGLYLYGVAPNANNVDAPEFVRLYKKNKMT 73  
DB 952 LPSGWTSNLTK-----SDNK-----NGSLAITGRVSNMNAQNSDITTFKV---SATDNV 996  
QY 74 QLTNLSKSKIONVGTVEHYVGDITDILFNSHQVLYKNNTYWGIIILANPQFIS 126  
DB 997 NNTTNSQSQKHV-----SIHYK-----ISEDAHPVLGNT--EKVVVNPTAVS 1039

RESULT 12  
US-09-757-041-2  
Sequence 2, Application US/09757041  
Patent No. US20020009726A1  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaaki  
TITLE OF INVENTION: CD40 Associated Proteins  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/757,041  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/349,357  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1203  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 543 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-757-041-2

Query Match 11.0%; Score 74; DB 9; Length 543;  
Best Local Similarity 28.3%; Pred. No. 23;  
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 21 ASSEPCVKNVSDW-----KLEILONGLYLYGVAPNAN---YNDVAPFEVRLYKKN 70  
DB 228 ASSAVGHVNLKREMSNLEKVSLLQV-----ESVERKNSISQHNQICSFLEIEROK 261  
QY 71 DMQLTNSKSKIONVGTVEHYVGDITDILFNSHQVLYK 109  
DB 282 EMLR--NNESKI-----LHLQRYVD---SQAEKLYK 306

RESULT 13  
US-10-004-378A-35  
Sequence 35, Application US/10004378A  
Publication No. US20030228301A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Furtak, Kazaryna  
APPLICANT: Perna, Amanda  
APPLICANT: Patuturajan, Meera  
APPLICANT: Shinkets, Richard A  
APPLICANT: Guo, Xiaojia Sasha  
APPLICANT: Casman, Stacie J  
APPLICANT: Burgess, Catherine E  
APPLICANT: Malysankar, Uriel M  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Vermet, Corrine A  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Agee, Michele  
APPLICANT: Rastelli, Luca  
APPLICANT: Shenoy, Suresh G  
APPLICANT: Grosse, William M  
APPLICANT: Alsobrook II, John P  
APPLICANT: Lepley, Denise M  
APPLICANT: Gerlach, Valerie  
APPLICANT: Edinger, Schlomit  
APPLICANT: MacDougall, John R  
APPLICANT: Peyman, John A  
APPLICANT: Gunther, Erik  
APPLICANT: Stone, David J  
APPLICANT: Ellerman, Karen  
APPLICANT: Gangolli, Beba A  
TITLE OF INVENTION: No. US20030228301A1 Human Proteins, Polynucleotides Encoding Th  
FILE REFERENCE: 21402-179  
CURRENT APPLICATION NUMBER: US/10/004,378A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 60/242,882  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,765  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/300,206  
PRIOR FILING DATE: 2001-06-22  
PRIOR APPLICATION NUMBER: 60/242,789  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,768  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,767  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/243,622  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 60/273,047  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 60/243,591  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 60/243,950  
PRIOR FILING DATE: 2000-10-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 191  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 35  
LENGTH: 543  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-004-378A-35

Query Match 11.0%; Score 74; DB 14; Length 543;  
Best Local Similarity 28.3%; Pred. No. 23;  
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 21 ASSEPPCVNKKVSDW-----KLEIIQNGLYLIYGVAPNAN---YNDVAPFEVRLYKXK 70  
DB 228 ASSAVQHVNLKEMNSLEKKVSLQN-----ESVEKNKSIQSLHNOICSPFEIEROK 281

QY 71 DMIQTLTKSKIQNVGTYELHVGDTIDLIENSEHOVLK 109  
DB 282 EMLR--NNESKI-----LHLQKVID----SQAEKXK 306

## RESULT 14

US-08-813-323A-1  
Sequence 1, Application US/08813323A  
Publication No. US20020031522A1

GENERAL INFORMATION:

APPLICANT: Baltimore, David  
APPLICANT: Cheng, Genhong  
APPLICANT: Cleary, Aileen  
APPLICANT: Lederer, Seth  
APPLICANT: Ye, Zheng-sheng  
TITLE OF INVENTION: TRUNCATED CRAPI INHIBITS CD40 SIGNALING  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/813,323A

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 50659

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 566 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..566

US-08-813-323A-1

Query Match 11.0%; Score 74; DB 8; Length 566;

Best Local Similarity 28.3%; Pred. No. 25;

Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

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DB 252 ASSAVQHVNLKEMNSLEKKVSLQN-----ESVEKNKSIQSLHNOICSPFEIEROK 305

QY 71 DMIQTLTKSKIQNVGTYELHVGDTIDLIENSEHOVLK 109  
DB 306 EMLR--NNESKI-----LHLQKVID----SQAEKXK 330

## RESULT 15

US-10-242-212-7

Sequence 7, Application US/10242212

Publication No. US2003009644A1

GENERAL INFORMATION:

APPLICANT: AHUJA, SEEMA

APPLICANT: BOWENWALD, LYNDIA

TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND

FILE REFERENCE: 4003.001000

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US/09/645,926

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patent version 3.0

SEQ ID NO 7

LENGTH: 567

TYPE: PRT

ORGANISM: Homo sapiens

US-10-242-212-7

Query Match 11.0%; Score 74; DB 14; Length 567;

Best Local Similarity 28.3%; Pred. No. 25;

Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

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DB 252 ASSAVQHVNLKEMNSLEKKVSLQN-----ESVEKNKSIQSLHNOICSPFEIEROK 305

QY 71 DMIQTLTKSKIQNVGTYELHVGDTIDLIENSEHOVLK 109  
DB 306 EMLR--NNESKI-----LHLQKVID----SQAEKXK 330

Search completed: November 2, 2004, 13:10:30  
Job time : 127 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2004, 12:52:52 ; Search time 461 Seconds  
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Title: US-10-080-455-1\_COPY\_52\_177

Perfect score: 675  
Sequence: 1 E7AKEPOMAKFGPLPSKQM.....VLKNTYWGIIILANPQFIS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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36: /cgn2\_6/ptodata/1/paa/US10 COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	675	100.0	169	1	PCT-US96-13282-2	Sequence 2, Appli
3	675	100.0	169	27	US-10-136-511-2	Sequence 2, Appli
4	675	100.0	177	1	PCT-US01-46625-3	Sequence 3, Appli
5	675	100.0	177	1	PCT-US02-16106-39	Sequence 39, Appli
6	675	100.0	177	1	PCT-US02-23782-40	Sequence 40, Appli
7	675	100.0	177	1	PCT-US02-25809-40	Sequence 40, Appli
8	675	100.0	177	15	US-09-195-368-1	Sequence 1, Appli
9	675	100.0	177	16	US-09-247-225-16	Sequence 16, Appli
10	675	100.0	177	20	US-09-613-972-14	Sequence 14, Appli
11	675	100.0	177	20	US-09-613-972-14	Sequence 14, Appli
12	675	100.0	177	26	US-10-080-455-1	Sequence 1, Appli
13	675	100.0	177	27	US-10-116-378-16	Sequence 16, Appli
14	675	100.0	177	27	US-10-151-882-39	Sequence 39, Appli
15	675	100.0	177	27	US-10-170-205E-28226	Sequence 28226, A
16	675	100.0	177	28	US-10-202-062-40	Sequence 40, Appli
17	675	100.0	177	28	US-10-218-547-40	Sequence 40, Appli
18	675	100.0	177	29	US-10-310-793-44	Sequence 44, Appli
19	675	100.0	177	30	US-10-405-027-3007	Sequence 3007, Ap
20	675	100.0	177	30	US-10-442-108-5	Sequence 5, Appli
21	675	100.0	177	33	US-10-713-391-1	Sequence 1, Appli
22	675	100.0	177	34	US-10-853-032-9	Sequence 9, Appli
23	608	90.1	113	29	US-10-338-083-17	Sequence 17, Appli
24	608	90.1	113	32	US-10-611-399-17	Sequence 17, Appli
25	566	83.9	508	1	PCT-US01-08631-47785	Sequence 47785, A
26	444	65.8	140	17	US-09-307-140-897	Sequence 897, App
27	444	65.8	140	23	US-09-817-076-897	Sequence 897, App
28	348	51.6	173	34	US-10-853-032-2	Sequence 2, Appli
29	84.5	12.5	1221	30	US-10-417-884-3959	Sequence 3959, Ap
30	84.5	12.5	1221	30	US-10-417-884-3959	Sequence 3959, Ap
31	78.5	11.7	32	36	US-60-581-351-10793	Sequence 10793, Ap
32	78.5	11.6	599	30	US-10-415-182A-1042	Sequence 1042, Ap
33	77	11.4	183	19	US-09-513-996A-54423	Sequence 54423, A
34	77	11.4	217	32	US-10-603-113-20671	Sequence 20671, A
35	77	11.4	217	36	US-60-096-409-20671	Sequence 20671, A
36	77	11.4	228	19	US-09-513-996A-54422	Sequence 54422, A
37	77	11.4	230	19	US-09-513-996A-54421	Sequence 54421, A
38	77	11.4	851	36	US-60-382-898-362	Sequence 362, App
39	76	11.3	2763	18	US-09-490-190-2	Sequence 2, Appli
40	75.5	11.2	314	22	US-08-791-537-120159	Sequence 120159, A
41	75.5	11.2	3829	12	US-08-827-356-5567	Sequence 5567, Ap
42	75.5	11.2	3829	20	US-09-611-529-4591	Sequence 4591, Ap
43	75.5	11.2	3829	25	US-09-950-084-4591	Sequence 4591, Ap
44	75.5	11.2	5795	1	PCT-US02-03987-12610	Sequence 12610, A
45	75.5	11.2	5795	23	US-09-815-242-12610	Sequence 12610, A

#### ALIGNMENTS

RESULT 1  
PCT-US00-04722-2  
Sequence 2, Appli  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: NI, Jian  
TITLE OF INVENTION: Human Endocrine Alpha and Methods of Use  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US00/04722
FILING DATE: 25-FEB-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/122,099
FILING DATE: 26-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/136,788
FILING DATE: 28-MAY-1999
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.047PC06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US00-04722-2

Query Match      100.0%; Score 675; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 8.3e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPCAKGRLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 60
DB 44 ETAKPCAKGRLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 103
QY 61 PFEVRLYNKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 120
DB 104 PFEVRLYNKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 163
QY 121 NPQFIS 126
DB 164 NPQFIS 169

RESULT 2
PCT-US96-13282-2
Sequence 2, Application PC/TUS9613282
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: 9410 Key West Avenue
APPLICANT: Rockville, MD 20850
APPLICANT: United States of America
APPLICANT: APPLICANTS/INVENTORS: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Endokine Alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13282
FILING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.047PC00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13282-2

Query Match      100.0%; Score 675; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 8.3e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPCAKGRLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 60
DB 44 ETAKPCAKGRLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 103
QY 61 PFEVRLYNKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 120
DB 104 PFEVRLYNKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 163
QY 121 NPQFIS 126
DB 164 NPQFIS 169

RESULT 3
US-10-136-511-2
Sequence 2, Application US/10136511
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
FILE REFERENCE: 1488.0470007/EKS/PSC
CURRENT APPLICATION NUMBER: US/10/136,511
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/513,584
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/345,790
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/136,788
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/122,099
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 08/912,227
PRIOR FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: 60/024,058
PRIOR FILING DATE: 1996-08-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 169
TYPE: PRT
ORGANISM: Homo sapiens
US-10-136-511-2

Query Match      100.0%; Score 675; DB 27; Length 169;
Best Local Similarity 100.0%; Pred. No. 8.3e-71;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPCAKGRLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 60
DB 44 ETAKPCAKGRLPSKQWASSEPPCVNKVSDMKLEILQNGLYLIYGQVAPNANYNDVA 103
QY 61 PFEVRLYNKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 120
DB 104 PFEVRLYNKMDIQLTNKSKIQNVGTYELHVGDTIDLIENSEHOVLKNTYWGIIILA 163
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QY 121 NPOFIS 126  
|||  
Db 164 NPOFIS 169

RESULT 4  
PCT-US01-46625-3

; Sequence 3, Application PC/TUS0146625  
; GENERAL INFORMATION:  
; APPLICANT: Genaisance Pharmaceuticals, Inc.  
; APPLICANT: Bentivegna, Steven C  
; APPLICANT: Bieglecki, Karyn M  
; APPLICANT: Sun, Xiao  
; TITLE OF INVENTION: HAPLOTYPES OF THE TNFSF18 GENE  
; FILE REFERENCE: TNFSF18 MMH-1787PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/46625  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: 60/247,501  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US01-46625-3

Query Match 100.0%; Score 675; DB 1; Length 177;  
Best Local Similarity 100.0%; Pred. No. 8,8e-71;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKPECMKFGPLPSKQWASSEPPCVNKVSDMKLEILLONGLYLYIGVAPNANYNDVA 60  
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Db 52 ETKPECMKFGPLPSKQWASSEPPCVNKVSDMKLEILLONGLYLYIGVAPNANYNDVA 111  
QY 61 PFEVRLYKXNDMIQTLTNKSKIQNVGTYELHVGDTIDLLFNSEHGVLLKNNYWGIIILLA 120  
|||  
Db 112 PFEVRLYKXNDMIQTLTNKSKIQNVGTYELHVGDTIDLLFNSEHGVLLKNNYWGIIILLA 171  
QY 121 NPOFIS 126  
|||  
Db 172 NPOFIS 177

RESULT 5  
PCT-US02-16106-39

; Sequence 39, Application PC/TUS0216106  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)  
; FILE REFERENCE: PFS54PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/16106  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293,100  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 39  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-16106-39

Query Match 100.0%; Score 675; DB 1; Length 177;  
Best Local Similarity 100.0%; Pred. No. 8,8e-71;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKPECMKFGPLPSKQWASSEPPCVNKVSDMKLEILLONGLYLYIGVAPNANYNDVA 60  
|||  
Db 52 ETKPECMKFGPLPSKQWASSEPPCVNKVSDMKLEILLONGLYLYIGVAPNANYNDVA 111  
QY 61 PFEVRLYKXNDMIQTLTNKSKIQNVGTYELHVGDTIDLLFNSEHGVLLKNNYWGIIILLA 120

Db 112 PFEVRLYKXNDMIQTLTNKSKIQNVGTYELHVGDTIDLLFNSEHGVLLKNNYWGIIILLA 171  
|||  
QY 121 NPOFIS 126  
|||  
Db 172 NPOFIS 177

RESULT 6  
PCT-US02-23782-40

; Sequence 40, Application PC/TUS0223782  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.,  
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members  
; FILE REFERENCE: PFS59PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/23782  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,838  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 40  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: human  
PCT-US02-23782-40

Query Match 100.0%; Score 675; DB 1; Length 177;  
Best Local Similarity 100.0%; Pred. No. 8,8e-71;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKPECMKFGPLPSKQWASSEPPCVNKVSDMKLEILLONGLYLYIGVAPNANYNDVA 60  
|||  
Db 52 ETKPECMKFGPLPSKQWASSEPPCVNKVSDMKLEILLONGLYLYIGVAPNANYNDVA 111  
QY 61 PFEVRLYKXNDMIQTLTNKSKIQNVGTYELHVGDTIDLLFNSEHGVLLKNNYWGIIILLA 120  
|||  
Db 112 PFEVRLYKXNDMIQTLTNKSKIQNVGTYELHVGDTIDLLFNSEHGVLLKNNYWGIIILLA 171  
QY 121 NPOFIS 126  
|||  
Db 172 NPOFIS 177

RESULT 7  
PCT-US02-25809-40

; Sequence 40, Application PC/TUS0225809  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel  
; FILE REFERENCE: PFS61PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/25809  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/312,542  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/330,761  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: human  
PCT-US02-25809-40

Query Match 100.0%; Score 675; DB 1; Length 177;  
Best Local Similarity 100.0%; Pred. No. 8,8e-71;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETKPECMKFGPLPSKQWASSEPPCVNKVSDMKLEILLONGLYLYIGVAPNANYNDVA 60  
|||  
Db 52 ETKPECMKFGPLPSKQWASSEPPCVNKVSDMKLEILLONGLYLYIGVAPNANYNDVA 111

Qy	61	PFVFRVRYKKKKMDIQLTNSKSIQLNGVGYEALHVGSTIDILINSEHQVLYKNNYTWGIILLA	120
Db	112	PFVFRVRYKKKKMDIQLTNSKSIQLNGVGYELAHVGSTIDILINSEHQVLYKNNYTWGIILLA	171
Qy	121	NPQFIS	126
Db	172	NPQFIS	177

RESULT 8  
US-09-195-368-1  
; Sequence 1, Application US/09195368A

```

1 GENERAL INFORMATION:
2 APPLICANT: Ashkenazi, Avi J.
3 APPLICANT: Baker, Kevin P.
4 APPLICANT: Godowski, Paul J.
5 APPLICANT: Gurney, Austin L.
6 APPLICANT: Mark, Melanie R.
7 APPLICANT: Masters, Scot A.
8 APPLICANT: Pitfi, Robert M.
9 TITLE OF INVENTION: DNA1935 Polypeptide, A Tumor Necrosis Factor Homolog
10 FILE REFERENCE: P115082
11 CURRENT APPLICATION NUMBER: US/09/195,368A
12 CURRENT FILING DATE: 1998-11-18
13 EARLIER APPLICATION NUMBER: US 60/069,661
14 EARLIER FILING DATE: 1997-12-12
15 EARLIER APPLICATION NUMBER: US 60/065,635
16 EARLIER FILING DATE: 1997-11-18
17 NUMBER OF SEQ ID NOS: 8
18 SEQ ID NO 1
19 LENGTH: 177
20 TYPE: ERT
21 ORGANISM: Homo sapiens
22 JS-09-195-368-1

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Query March	100.0%	Score 675;	DB 15;	Length 177;
Best Local Similarity	100.0%;	Pred. NO. 8.8e-71;		
Matches 126;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 ETAKECCKMAKFGFLPCKWMASSBPCKVKSVDWLTETLQNGLYLITGOVAPANNAYDVA 60  
Db 52 ETAKECCKMAKFGFLPCKWMASSBPCKVKSVDWLTETLQNGLYLITGOVAPANNAYDVA 111  
QY 61 PEPEVRVYKXKMDCTLTNSKTIQNGGYEALHVGDTLPIENSEHOKKONTWGIITLA 120  
Db 112 PEPEVRVYKXKMDCTLTNSKTIQNGGYEALHVGDTLPIENSEHOKKONTWGIITLA 171  
QY 121 NPOFIS 126  
Db 172 NPOFIS 177

RESULT 9  
US-09-247-225-16  
; Sequence 16, Application US/09247225A

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1 GENERAL INFORMATION:
2 APPLICANT: Ashkenazi, Avi J.
3 APPLICANT: Goddard, Audrey
4 APPLICANT: Guiney, Austin
5 APPLICANT: Marsters, Scot A.
6 APPLICANT: Pitti, Robert M.
7 APPLICANT: Wood, William
8 TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
9 TITLE OF INVENTION: ACIDS ENCODING THE SAME
10 FILE REFERENCE: P1206R1
11 CURRENT APPLICATION NUMBER: US/09/247,225A
12 CURRENT FILING DATE: 1999-02-09
13 EARLIER APPLICATION NUMBER: US 60/074,087
14 EARLIER FILING DATE: 1998-02-09
15 NUMBER OF SEQ ID NOS: 31
16 SEQ ID NO 16
17 LENGTH: 177

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-247-225-16

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Query Match	100.0%	Score 675;	DB 16	Length 177;
Best Local Similarity	100.0%	Pred. No. 8.8e-71;		
Matches 126;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ETAKBECMAKFBPLPSKQWMASSBEPCCNKAISDWLLETILQNGLYLIGQVAPNANYDVA 60  
Db 52 ETAKBECMAKFBPLPSKQWMASSBEPCCNKAISDWLLETILQNGLYLIGQVAPNANYDVA 1:1:1  
QY 61 PEEVRLYRKXKMDIQTLLNKSKITQNGYGYEYELHVGDTIDLINSEHQLKXNTTWIGIILLA 120  
Db 112 PEEVRLYRKXKMDIQTLLNKSKITQNGYGYEYELHVGDTIDLINSEHQLKXNTTWIGIILLA 171  
QY 121 NPQFIS 126  
Db 172 NPQFIS 177

RESULT 10  
US-09-613-972-14  
; Sequence 14, Application US/09613972

```

/ GENERAL INFORMATION:
/ APPLICANT: P. Mickey Williams
/ APPLICANT: Mary E. Gettelsen
/ TITLE OF INVENTION: PROMOTION OR INHIBITION OF ANGIOGENESIS AND
/ TITLE OF INVENTION: CARDIOVASCULARIZATION BY TUMOR NECROSIS FACTOR
/ FILE REFERENCE: P1765R1
/ CURRENT APPLICATION NUMBER: US/09/613,972
/ CURRENT FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: US 60/143,304
/ PRIOR FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 22
/ SEQ ID NO 14
/ LENGTH: 177
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-613-972-14

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Query March	100.0%;	Score 675;	DB 20;	Length 177;
Best Local Similarity	100.0%;	Pred. No. 8.8e-71;		
Matches 126; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	ETAKPECMKAPBPLBSKKOMASSEPPCYNKYSIDWKEITLQNGKLTILGQVAPNNYNDVA	60
Db	52	ETAKPECMKAPBPLBSKKOMASSEPPCYNKYSIDWKEITLQNGKLTILGQVAPNNYNDVA	111
Qy	61	PEFVRLRYKKKMDIQLTNKSKTQNGYGTVEHVGDTDLLFNSEHQVAKNTYWGILLIA	120
Db	112	PEFVRLRYKKKMDIQLTNKSKTQNGYGTVEHVGDTDLLFNSEHQVAKNTYWGILLIA	171
Qy	121	NPOFIS 126	
Db	172	NPOFIS 177	

RESULT 11  
US-09-613-972A-14  
; Sequence 14, Application US/09613972A

GENERAL INFORMATION:  
APPLICANT: P. Mickey Williams  
APPLICANT: Mary E. Gerilsen  
TITLE OF INVENTION: PROMOTION OR INHIBITION OF ANGIOGENESIS AND  
TITLE OF INVENTION: CARBOXYMETHYLATION BY TUMOR NECROSIS FACTOR  
TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS  
FILE REFERENCE: 91765R1  
CURRENT APPLICATION NUMBER: US/09/613,972A  
CURRENT FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: US 60/143,304  
PRIOR FILING DATE: 1999-07-12

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; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 14
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-613-972A-14

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Query Match	100.0%	Score 675	DB 20	Length 177
Best Local Similarity	100.0%	Pred. No. 8.8e-71		
Matches 126	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 ETAKPECMKAFGFLPEKQWMASSPEPCVAKVSDMKLTLLQNGLYITIGQVAPNNAYDVA 60  
 Db 52 ETAKPECMKAFGFLPEKQWMASSPEPCVAKVSDMKLTLLQNGLYITIGQVAPNNAYDVA 111  
 QY 61 PEPEVRLYRKNDMQLTLNKSQTLQNGYIEHVGOTDILINSEHOUVAKNTYAGTITLLA 120  
 Db 112 PEPEVRLYRKNDMQLTLNKSQTLQNGYIEHVGOTDILINSEHOUVAKNTYAGTITLLA 171

QY	121	NPQFIS	126
Db	172	NPQFIS	177

RESULT 12  
US-10-080-455-1

GENERAL INFORMATION:  
Sequence 1#, Application US/10080455  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Mark, Melanie R.  
APPLICANT: Masters, Scott A.

10 TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog

CURRENT APPLICATION NUMBER: US/10/080,455

PRIOR APPLICATION NUMBER: 09/1995,368

PRIOR FILING DATE: 1997-12-12

PRIOR FILING DATE: 1997-11-18

NUMBER OF SEQ ID NOS: 8  
: SEQ ID NO 1

TYPE: PRT

US-10-080-455-1

Query Match	100.0%	Score 675; DB 26;	Length 177;
Best Local Similarity	100.0%	Pred. No. 8, 8e-71;	
Matches 126; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;

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QY 61 PFEVRLYKXNDMIQTLTNKSKIQNNGTGYELHVGDTDLINSEHQVLKNNFTYGIILLA 1200  
 112 PFEVRLYKXNDMIQTLTNKSKIQNNGTGYELHVGDTDLINSEHQVLKNNFTYGIILLA 1711  
 DQ

QY	121	NPQFIS	126
Db	172	NPQFIS	177

RESULT 13  
US-10-116-378-16

; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin  
APPLICANT: Masters, Scot A.  
APPLICANT: Pitti, Robert M.  
APPLICANT: Wood, William

```

: TITLE OF INVENTION: NUCLEIC
:
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
:
: FILE REFERENCE: P1206R1

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1 CURRENT FILING DATE: 2002-04-04 APPLICATION NUMBER: 09/247,225
2 PRIOR APPLICATION NUMBER: EARLIER
3 PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
4 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,088
5 PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
6 NUMBER OF SEQ ID NOS: 31
7
8 SEQ ID NO 16
9

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-16

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Query Match	100.0%	Score 675;	DB 27;	Length 177;
Best Local Similarity	100.0%	Pred. No. 8.8e-71;		
Matches 126; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 ETAAEPCMAKFGPLPSKMQMASSEPPCVNKKVSDMKLELLQNGLYLYIGQVAPNANYNDA 600

Db 52 ETAAEPCMAKFGPLPSKMQMASSEPPCVNKKVSDMKLELLQNGLYLYIGQVAPNANYNDA 11

QY 61 PFEVRLYNKKMDIQTLLTNKSKIQNVGTYELHVGPTIDLINSEHQVLKNNTYWGIILLA 120  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 112 PFEEVRLYNKKMDIQTLTNKSKIQNVGTYELHVGPTIDLINSEHQVLKNNTYWGIILLA 171

QY	121	NPQFIS	126
Db	172	NPQFIS	177

RESULT 14  
US-10-151-882-39  
: Sequence 39 Application IIS/10151882

APPLICANT: Ruben. Steven M.

FILE REFERENCE: PF554

CURRENT FILING DATE: 2002-05-22

PRIOR FILING DATE: 2001-05-24

; SOFTWARE: PatentIn version 3.0

LENGTH: 177

ORGANISM: Homo sapiens  
US-10-151-882-39

Best Local Similarity 100.0%; Pred. No. 8, 8e-71;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

52 ETAKPECMATKFGPLPSKQWASSEPPCVNKVSPMKLEILQNGJYLIGQVAPNANYNDVA 11

112 PFERLYKKMDIQLTNKSKIQVVGTYELHVGDTIDLFNSEHQLKNNTYWGIILDA 171

[illegible]

Db 172 NPOFIS 177

RESULT 15  
US-10-170-205E-28226

; Sequence 28226, Application US/10170205E

; GENERAL INFORMATION:

; APPLICANT: ADAMS, Mark

; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN

; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

; FILE REFERENCE: C1001381

; CURRENT APPLICATION NUMBER: US/10/170,205E

; CURRENT FILING DATE: 2002-06-13

; NUMBER OF SEQ ID NOS: 40312

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 28226

; LENGTH: 177

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-170-205E-28226

Query Match 100.0%; Score 675; DB 27; Length 177;

Best local Similarity 100.0%; Pred. No. 8.8e-71;

Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ETAKEPCMAKFGPLPSKWMASBPVCVNSDKLEILQNGLYLYGVAPNANYNDVA	60
Db	52	ETAKEPCMAKFGPLPSKWMASBPVCVNSDKLEILQNGLYLYGVAPNANYNDVA	111
QY	61	PFEVRLYNKMDMIQTLTNKSKIQNVGTYELHWGDTIDLFNSEHQVLKNNYWGIIILA	120
Db	112	PFEVRLYNKMDMIQTLTNKSKIQNVGTYELHWGDTIDLFNSEHQVLKNNYWGIIILA	171
QY	121	NPOFIS 126	
Db	172	NPOFIS 177	

Search completed: November 2, 2004, 13:08:00  
Job time : 462 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: November 2, 2004, 12:55:37 ; Search time 12 Seconds  
(without alignments)  
57.744 Million cell updates/sec

Title: US-10-080-455-1\_COPY\_52\_177

Perfect score: 675  
Sequence: 1 ETAKERCMAKFGPLPSKMQM.....VLKNTYWGIIILANPQFIS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 40726 seqs, 5499444 residues

Total number of hits satisfying chosen parameters: 40726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/prodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/paa/US09\_NEW\_COMB.pep:\*  
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7: /cgn2\_6/prodata/1/paa/US11\_NEW\_COMB.pep:\*  
8: /cgn2\_6/prodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	675	100.0	177	6	US-10-959-537-16
2	608	90.1	113	6	US-10-794-751-17
3	70.5	10.4	137	6	US-10-220-366A-15820
4	68	10.1	840	6	US-10-952-698-181
5	67.5	10.0	317	6	US-10-948-576-145
6	67	9.9	285	6	US-10-955-952-24
7	67	9.9	285	6	US-10-157-779-24
8	67	9.9	285	6	US-10-964-241-24
9	67	9.9	285	6	US-10-626-914-9
10	66.5	9.9	525	6	US-10-076-157A-11
11	64	9.5	157	6	US-10-668-178-15
12	64	9.5	157	6	US-10-668-178-16
13	64	9.5	307	6	US-10-948-576-122
14	64	9.5	307	6	US-10-948-576-123
15	64	9.5	307	6	US-10-948-576-135
16	63.5	9.4	141	6	US-10-794-751-8
17	63.5	9.4	259	8	US-60-613-702-11
18	63	9.3	147	6	US-10-794-751-1
19	63	9.3	150	6	US-10-959-537-28
20	63	9.3	157	6	US-10-668-178-1
21	63	9.3	157	6	US-10-957-134-1
22	63	9.3	157	6	US-10-957-134-1
23	63	9.3	157	6	US-10-957-134-1
24	63	9.3	233	1	PCT-US04-31524-147
25	62.5	9.3	322	6	US-10-948-576-138

26	62	9.2	157	6	US-10-668-178-2	Sequence 2, App1
27	61	9.0	122	6	US-10-970-713-286	Sequence 286, App
28	60.5	9.0	214	6	US-10-970-713-306	Sequence 306, App
29	60.5	9.0	274	6	US-10-948-576-144	Sequence 144, App
30	60.5	9.0	301	6	US-10-948-576-142	Sequence 142, App
31	60.5	9.0	322	6	US-10-948-576-128	Sequence 128, App
32	60.5	9.0	322	6	US-10-948-576-129	Sequence 129, App
33	60.5	9.0	349	6	US-10-948-576-139	Sequence 139, App
34	60.5	9.0	884	6	US-10-900-231-5	Sequence 157, App
35	60	8.9	170	5	US-09-791-153D-157	Sequence 141, App
36	60	8.9	259	6	US-10-948-576-141	Sequence 2, App1
37	60	8.9	489	6	US-10-958-008-2	Sequence 801, App
38	60	8.9	1021	6	US-10-399-103A-801	Sequence 4, App1
39	60	8.9	1031	1	PCT-US04-16942-4	Sequence 5, App1
40	60	8.9	1114	1	PCT-US04-16942-5	Sequence 9, App1
41	59.5	8.8	141	6	US-10-794-751-9	Sequence 3, App1
42	59	8.7	157	6	US-10-668-178-3	Sequence 121, App
43	59	8.7	157	6	US-10-668-178-13	Sequence 134, App
44	59	8.7	307	6	US-10-948-576-121	
45	59	8.7	307	6	US-10-948-576-134	

## ALIGNMENTS

RESULT 1  
US-10-959-537-16  
; Sequence 16, Application US/10959537  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin  
; APPLICANT: Maestri, Scott A.  
; APPLICANT: Bitzi, Robert M.  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGY AND NUCLEIC  
; FILE REFERENCE: P1206R1  
; CURRENT APPLICATION NUMBER: US/10/959,537  
; CURRENT FILING DATE: 2004-10-06  
; PRIOR APPLICATION NUMBER: US/09/247,225  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: US 60/074,087  
; PRIOR FILING DATE: 1998-02-09  
; NUMBER OF SEQ ID NOS: 31  
; SEQ ID NO 16  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-959-537-16  
Query Match 100.0%; Score 675; DB 6; Length 177;  
Best Local Similarity 100.0%; Pred.No.1.4e-69;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ETAKERCMAKFGPLPSKMQMASSEPCVANKVSDMKLEIIQNGHYLYLYGQVAPNANYDVA 60  
Db 52 ETAKERCMAKFGPLPSKMQMASSEPCVANKVSDMKLEIIQNGHYLYLYGQVAPNANYDVA 111  
QY 61 PFEVRLYKXKDMIQTLTNSKIQNVGCTYELHVGDTIIDLIFNSEHOVLKNTYWGIIILA 120  
Db 112 PFEVRLYKXKDMIQTLTNSKIQNVGCTYELHVGDTIIDLIFNSEHOVLKNTYWGIIILA 171  
QY 121 NPQFIS 126  
Db 172 NPQFIS 177  
RESULT 2  
US-10-794-751-17  
; Sequence 17, Application US/10794751  
; GENERAL INFORMATION:  
; APPLICANT: Desjarlais, John R.

```
; APPLICANT: Thomson, Adam Read
; APPLICANT: Zhukovsky, Eugene Alexander
; TITLE OF INVENTION: BAFV VARIANTS AND METHODS THEREOF
; FILE REFERENCE: A-72175-1
; CURRENT APPLICATION NUMBER: US/10/794,751
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/452,707
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/482,081
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/523,880
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 60/528,104
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-751-17
```

```
Query Match          90.1%; Score 608; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 3e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 CMAKFGPLPSKQWASSPPCVNKVSDMKLEILONGLYLYIGQVAPNNYNDVAPFEVRL 66
DB 1 CMAKFGPLPSKQWASSPPCVNKVSDMKLEILONGLYLYIGQVAPNNYNDVAPFEVRL 60
QY 67 YKNDMTQTLNKSCKIQWVGTYELHVGDTIDLFNSHQVLKNTYWGIIIL 119
DB 61 YKNDMTQTLNKSCKIQWVGTYELHVGDTIDLFNSHQVLKNTYWGIIIL 113
```

## RESULT 3

```
US-10-220-366A-15820
; Sequence 15820, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSERQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 15820
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(137)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-15820
```

```
Query Match          10.4%; Score 70.5; DB 6; Length 137;
Best Local Similarity 30.0%; Pred. No. 0.25;
Matches 30; Conservative 13; Mismatches 38; Indels 19; Gaps 5;
```

```
QY 36 LEILONGLYLYIGQVAPNNYND-VAPFEVRLYKNDMTQTLNKSCKIQWVGTYELH-V 93
DB 47 LSIQVG---VHRSLAAMTFALIVTP-----NIDSLQELVVRGNSQYRGAKYIIRDN 97
QY 94 GDTIDLFNSHQVLKNTYW-----GIIILANPOFI 125
DB 98 GDRIDLRHFGHSDLHLQTYGVKVRHMCDDGDIVIFNRQCI 137
```

```
RESULT 4
US-10-952-698-181
; Sequence 181, Application US/10952698
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/952,698
; CURRENT FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 181
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-952-698-181
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```
Query Match          10.1%; Score 68; DB 6; Length 840;
Best Local Similarity 18.2%; Pred. No. 5.2;
Matches 24; Conservative 31; Mismatches 35; Indels 42; Gaps 5;
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```
QY 7 CMAKFGPLPSKQWASSPPCVNKVSDMKLEILONGLYLYI-----GGVAPNNYND 58
DB 48 CEAKGIRKVSISVPSRP-----FQSLNNGLTMLHTNDPSGLTNALISHLGRNN 99
QY 59 VAPFEVRLYKNDMTQTLNKSCKIQWVGTYELHVGDTIDLFNSHQVLKNTYWGII-- 116
DB 100 IADIEIGAFNGELGLK-----QLHIN-----HNSLEILKEDPFPHGEN 137
QY 117 --IILANPOFIS 126
DB 138 LEFLQADNNFYIT 149
```

## RESULT 5

```
US-10-948-576-145
; Sequence 145, Application US/10948576
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; BAUER, S. C.
; BRADFORD-GOLDBERG, SARAH R.
; CAPARON, MAIRE H.
; EASTON, ALAN M.
; KLEIN, BARBARA K.
; MCKEARN, JOHN P.
; OLINS, PETER O.
; PAIK, KUMMAN
; THOMAS, JOHN W.
; TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
; Using Multivariant IL-3 Hematopoietic Chimera Proteins
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Carol M. Nielsen, Winstead Sechrest & Minick P.C.
; STREET: P.O. Box 50784
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/948,576
; FILING DATE: 22-Sep-2004
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/083,446
```

FILED DATE: 22-FEB-2002  
APPLICATION NUMBER: 08/762,227  
FILING DATE: 09-DEC-1996  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: US 08/446,872  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Carol M. Nielsen  
REGISTRATION NUMBER: 37,676  
REFERENCE/DOCKET NUMBER: 2790/7 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-650-2722  
TELEFAX: 214-745-5390  
INFORMATION FOR SEQ ID NO: 145:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 317 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 145:  
US-10-948-576-145

Query Match 10.0%; Score 67.5; DB 6; Length 317;  
Best Local Similarity 28.0%; Pred. No. 1.6;  
Matches 28; Conservative 12; Mismatches 27; Indels 33; Gaps 6;

QY 5 EPQMAKFGPLPSKQWASPPCVNKVS-----LETLNGLYITGVAP 52  
DB 70 QPC-----LPSSA-TAPASHPIIYAGDWQEFREKLTFLVLTLEQAEQYVIEGRISP 122

QY 53 -----NANYNDVAFPEVRLYKNKMI-----OTLTNKSRI 82  
DB 123 GGGGGGGGSMAPVPGS-----DSKDVAAAPHPRLTSSERI 158

RESULT 6  
US-10-955-952-24

Sequence 24, Application US/10955952  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C12  
CURRENT APPLICATION NUMBER: US/10/955,952  
CURRENT FILING DATE: 2004-09-29  
PRIOR APPLICATION NUMBER: US/10/121,058  
PRIOR FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 24  
LENGTH: 285  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-955-952-24

Query Match 9.9%; Score 67; DB 6; Length 285;  
Best Local Similarity 22.2%; Pred. No. 1.6;  
Matches 35; Conservative 20; Mismatches 51; Indels 52; Gaps 7;

QY 1 ETAKPQNAKFGPLPSKQWASPPCVNKVS-----DW-----KLEILON 41  
DB 140 ETVTDQCLQ-----LIADSEPTTQKSGSYTFVFWPLSPKSGALBEKENKIIVKET 190

QY 42 GLYLYGGVAPNANYNDVAFPEVRLYKNK-----DMITLTNKSRIQNV----- 85  
DB 191 GTFPIYGOVL-----YTDKYAMGHILQKRVHVGDELSVTLFRCTQMPPTLPNNSC 246

QY 86 -GGTYLHVGDITDILFENSEHVLK-----NNTYWGIIIL 119  
DB 247 SAGIAKLBEGDELQLAIPRENNQISLDGVTFFGALKL 284

RESULT 7  
US-10-157-779-24

Sequence 24, Application US/10157779  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C426  
CURRENT APPLICATION NUMBER: US/10/157,779  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17

```

; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-157-779-24

Query Match
Best Local Similarity 22.2%; Pred. No. 1.6;
Matches 35; Conservative 20; Mismatches 51; Indels 52; Gaps 7;

QY 1 ETAKPCMAKGPRLPSKQWASSPPCVNKVS---DW-----KLEIION 41
Db 140 ETVYQDCLQ-----LIADSEPTTIQKGSYTFVFWLSPKGSALAEKENKILVKET 190
QY 42 GLVLIYQVAPNANYNDVAPPEVRLYNNK-----DMIQTLTNKSKIONV----- 85
Db 191 GYFFIYQVVL-----YTDKTYAMGHILQKRVHVGDELSTVTLFRCIQNMPEITLPNNSCY 246

QY 86 -GGTYELHVGDTIDLIENSEHOVVK--NNTYWGIIILL 119
Db 247 SAGIAKLEEGDELQALIPRENAQISLDGDVYFFGALKI 284

RESULT 8
US-10-964-241-24
; Sequence 24, Application US/10964241
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gutney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zenith
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C33
; CURRENT APPLICATION NUMBER: US/10/964,241
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PRIORT APPLICATION NUMBER: US/10/123,236
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
```

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; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-964-241-24

Query Match
Best Local Similarity 22.2%; Pred. No. 1.6;
Matches 35; Conservative 20; Mismatches 51; Indels 52; Gaps 7;

QY 1 ETAKPCMAKGPRLPSKQWASSPPCVNKVS---DW-----KLEIION 41
Db 140 ETVYQDCLQ-----LIADSEPTTIQKGSYTFVFWLSPKGSALAEKENKILVKET 190
QY 42 GLVLIYQVAPNANYNDVAPPEVRLYNNK-----DMIQTLTNKSKIONV----- 85
Db 191 GYFFIYQVVL-----YTDKTYAMGHILQKRVHVGDELSTVTLFRCIQNMPEITLPNNSCY 246

QY 86 -GGTYELHVGDTIDLIENSEHOVVK--NNTYWGIIILL 119
Db 247 SAGIAKLEEGDELQALIPRENAQISLDGDVYFFGALKI 284

RESULT 9
US-10-626-914-9
; Sequence 9, Application US/10626914
; GENERAL INFORMATION:
; Applicant: Chuntcharapai, Annan
; Applicant: Docket Preview
; Applicant: GREWAL, IOBAL
; Applicant: KIM, KYUNG JIN
; Applicant: YAN, MINHONG
; TITLE OF INVENTION: TACT Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-9

Query Match
Best Local Similarity 22.2%; Pred. No. 1.6;
Matches 35; Conservative 20; Mismatches 51; Indels 52; Gaps 7;

QY 1 ETAKPCMAKGPRLPSKQWASSPPCVNKVS---DW-----KLEIION 41
Db 140 ETVYQDCLQ-----LIADSEPTTIQKGSYTFVFWLSPKGSALAEKENKILVKET 190
QY 42 GLVLIYQVAPNANYNDVAPPEVRLYNNK-----DMIQTLTNKSKIONV----- 85
Db 191 GYFFIYQVVL-----YTDKTYAMGHILQKRVHVGDELSTVTLFRCIQNMPEITLPNNSCY 246

QY 86 -GGTYELHVGDTIDLIENSEHOVVK--NNTYWGIIILL 119
Db 247 SAGIAKLEEGDELQALIPRENAQISLDGDVYFFGALKI 284

RESULT 10
US-10-076-157A-11
; Sequence 11, Application US/10076157A
```



```
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Seubberger, Harald
/ APPLICANT: Hoeffken, Hans Wolfgang
/ APPLICANT: Doval, Jose Luis Revuelta
/ APPLICANT: Jimenez, Alberto
/ APPLICANT: Garcia, Maria Angeles Santos
/ TITLE OF INVENTION: Phosphoriboxyl-Pyrophosphate Synthetase Polypeptide
/ FILE REFERENCE: PP46687-2/DP
/ CURRENT APPLICATION NUMBER: US/10/076,157A
/ PRIOR FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: Germany, 1975775.5
/ PRIOR FILING DATE: 1997-12-23
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: WordPerfect 8
/ SEQ ID NO 11
/ LENGTH: 525
/ TYPE: PRT
/ ORGANISM: Asibhya gossypii
US-10-076-157A-11
```

```
Query Match          9.9%; Score 66.5; DB 6; Length 525;
Best Local Similarity 27.4%; Pred. No. 4.1;
Matches 29; Conservative 16; Mismatches 32; Indels 29; Gaps 7;
```

```
QY 26 PCVNAKUSD--WKLE--ILQNGLYLYIGVAPNANNDVAPFEVRL-----YKXKDMICIT 75
DB 42 PCTQKISELQMKKXVILSGPYSVVAADAPHV--DRANFELGVPLIGTCYGLQELAMT 98
QY 76 LNKSKIQNVG-----GTVELHVGDTIDLINSEHOVLKNNTYW 114
DB 99 AG-----AEVGRGKREYGRATLHVDSACPLFNN-----VDSSTW 135
```

```
RESULT 11
/ Sequence 15, Application US/10668178
/ GENERAL INFORMATION:
/ APPLICANT: KAMUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
/ APPLICANT: MAYUMI, Tadanoiri
/ APPLICANT: TSUTSUMI, Yasuo
/ APPLICANT: NAKAGAWA, Shinsaku
/ APPLICANT: IKEGAMI, Hakuo
/ TITLE OF INVENTION: Biologically-active conjugate
/ FILE REFERENCE: MAYUMI2A
/ CURRENT APPLICATION NUMBER: US/10/668,178
/ PRIOR FILING DATE: 2003-09-24
/ PRIOR APPLICATION NUMBER: JP 83509/2002
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: JP 185387/2002
/ PRIOR FILING DATE: 2002-06-26
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 15
/ LENGTH: 157
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic Construct
US-10-668-178-15
```

```
Query Match          9.5%; Score 64; DB 6; Length 157;
Best Local Similarity 21.5%; Pred. No. 1.6;
Matches 26; Conservative 21; Mismatches 38; Indels 36; Gaps 5;
```

```
QY 30 KVSMDKLEILQNGLYLYIGV-----APNANY--NDVAPFEVRLYKXKDMIQTLTKNS 80
DB 42 ELRDNQLVVPSSEGLYLYISQVLFSGGCPSTHVLTHHTISRIVSYQTRVNLISALASPC 101
QY 81 KIQN-----VGTVELHVGDTID-----LINSEHOVLKNNTYWGIIL 118
DB 102 QRETPGAEALPWYEPYLYIGVQLETGDRLSAEINRPDYLDPAESGQV-----YFGIILA 156
```

```
QY 119 L 119
DB 157 L 157
```

```
RESULT 12
/ Sequence 16, Application US/10668178
/ GENERAL INFORMATION:
/ APPLICANT: KAMUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
/ APPLICANT: MAYUMI, Tadanoiri
/ APPLICANT: TSUTSUMI, Yasuo
/ APPLICANT: NAKAGAWA, Shinsaku
/ APPLICANT: IKEGAMI, Hakuo
/ TITLE OF INVENTION: Biologically-active conjugate
/ FILE REFERENCE: MAYUMI2A
/ CURRENT APPLICATION NUMBER: US/10/668,178
/ PRIOR FILING DATE: 2003-09-24
/ PRIOR APPLICATION NUMBER: JP 83509/2002
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: JP 185387/2002
/ PRIOR FILING DATE: 2002-06-26
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 16
/ LENGTH: 157
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: synthetic (Variant protein of human tumor necrosis factor)
US-10-668-178-16
```

```
Query Match          9.5%; Score 64; DB 6; Length 157;
Best Local Similarity 21.5%; Pred. No. 1.6;
Matches 26; Conservative 21; Mismatches 38; Indels 36; Gaps 5;
```

```
QY 30 KVSMDKLEILQNGLYLYIGV-----APNANY--NDVAPFEVRLYKXKDMIQTLTKNS 80
DB 42 ELRDNQLVVPSSEGLYLYISQVLFSGGCPSTHVLTHHTISRIVSYQTRVNLISALASPC 101
QY 81 KIQN-----VGTVELHVGDTID-----LINSEHOVLKNNTYWGIIL 118
DB 102 QRETPGAEALPWYEPYLYIGVQLETGDRLSAEINRPDYLDPAESGQV-----YFGIILA 156
QY 119 L 119
DB 157 L 157
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RESULT 13
/ Sequence 122, Application US/10948576
/ GENERAL INFORMATION:
/ APPLICANT: Abrams, Mark A.
/ APPLICANT: Bauer, S. C.
/ APPLICANT: Braford-Goldberg, Sarah R.
/ APPLICANT: Caparon, Mairé H.
/ APPLICANT: Easton, Alan M.
/ APPLICANT: Klein, Barbara K.
/ APPLICANT: McKeatn, John P.
/ APPLICANT: Olin, Peter O.
/ APPLICANT: Paik, Kumman
/ APPLICANT: Thomas, John W.
/ TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
/ USING Multivariant IL-3 Hematopoiesis Chimera Proteins
/ NUMBER OF SEQUENCES: 197
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Carol M. Nielsen, Winstead Sechrest & Minick P.C.
/ STREET: P.O. Box 50784
/ CITY: Dallas
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 75201
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/948,576
FILING DATE: 22-Sep-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/083,446
FILING DATE: 22-FEB-2002
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carol M. Nielsen
REGISTRATION NUMBER: 37,676
REFERENCE/DOCKET NUMBER: 2790/7 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-650-2722
TELEFAX: 214-745-5390
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 122:
US-10-948-576-122

Query Match          9.5%; Score 64; DB 6; Length 307;
Best Local Similarity 25.9%; Pred. No. 3.9;
Matches 29; Conservative 11; Mismatches 40; Indels 32; Gaps 5;

QY 5 EPCMAKGPSPSKQWMASSPPCVNKSVDK-----LEIDNGILYLYGVAP 52
DB 70 QPC-----LESA-TAAPSRRPITIKAGDWQEFREKLTFLYVLTLEQAQEQGVLEGRISP 122

QY 53 NANYNDVAFPEVRLYKKNKMIQTLTNKS-----KIQWVG-----GTVEL 91
DB 123 GGGSGGGSNMPTLGPASSLPGPSFLKSLBQYRKIQGDAALQKCATYTL 174

RESULT 14
US-10-948-576-123
Sequence 123, Application US/10948576
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Bratford-Goldberg, Sarah R.
Caparon, Maïre H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant IL-3 Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESSES:
ADDRESSSEE: Carol M. Nielsen, Winstead Secrest & Minick P.C.
STREET: P.O. Box 50784
CITY: Dallas
STATE: Texas
COUNTRY: USA
ZIP: 75201
COMPUTER READABLE FORM:
MEDIUM TYPE: CD
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MEDIUM TYPE: CD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/948,576
FILING DATE: 22-Sep-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/083,446
FILING DATE: 22-FEB-2002
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carol M. Nielsen
REGISTRATION NUMBER: 37,676
REFERENCE/DOCKET NUMBER: 2790/7 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-650-2722
TELEFAX: 214-745-5390
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-10-948-576-123

Query Match          9.5%; Score 64; DB 6; Length 307;
Best Local Similarity 25.9%; Pred. No. 3.9;
Matches 29; Conservative 11; Mismatches 40; Indels 32; Gaps 5;

QY 5 EPCMAKGPSPSKQWMASSPPCVNKSVDK-----LEIDNGILYLYGVAP 52
DB 70 QPC-----LESA-TAAPSRRPITIKAGDWQEFREKLTFLYVLTLEQAQEQGVLEGRISP 122

QY 53 NANYNDVAFPEVRLYKKNKMIQTLTNKS-----KIQWVG-----GTVEL 91
DB 123 GGGSGGGSNMPTLGPASSLPGPSFLKSLBQYRKIQGDAALQKCATYTL 174

RESULT 15
US-10-948-576-135
Sequence 135, Application US/10948576
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Bratford-Goldberg, Sarah R.
Caparon, Maïre H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant IL-3 Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESSES:
ADDRESSSEE: Carol M. Nielsen, Winstead Secrest & Minick P.C.
STREET: P.O. Box 50784
CITY: Dallas
STATE: Texas
COUNTRY: USA
ZIP: 75201
COMPUTER READABLE FORM:
MEDIUM TYPE: CD
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1 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: PC-DOS/MS-DOS
3 SOFTWARE: Patent In Release #1.0, Version #1.25
4
5 CURRENT APPLICATION NUMBER: US/10/948,576
6 FILING DATE: 22-Sep-2004
7 CLASSIFICATION: <Unknown>
8
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 10/083,446
11 FILING DATE: 22-FEB-2002
12 APPLICATION NUMBER: 08/762,227
13 FILING DATE: 09-DEC-1996
14 APPLICATION NUMBER: US 08/192,325
15 FILING DATE: 14-FEB-1994
16 APPLICATION NUMBER: US 08/446,872
17 FILING DATE: 06-JUN-1995
18
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Carol M. Nielsen
21 REGISTRATION NUMBER: 37,676
22 REFERENCE/DOCKET NUMBER: 2790/7 US
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 713-650-2722
25 TELEFAX: 214-745-5390
26 INFORMATION FOR SEQ ID NO: 135:
27 SEQUENCE CHARACTERISTICS:
28     LENGTH: 307 amino acids
29     TYPE: amino acid
30     STRANDEDNESS: <Unknown>
31     TOPOLOGY: linear
32 MOLECULE TYPE: protein
33 SEQUENCE DESCRIPTION: SEQ ID NO: 135:
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35 US-10-948-576-135
36
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38 Best Local Similarity 25.9%; Pred. No. 3.9;
39 Matches 29; Conservative 11; Mismatches 40; Indels 32; Gaps 5
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Job time : 13 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2004, 12:50:22 ; Search time 38 Seconds

(without alignments)  
319.035 Million cell updates/sec

Title: US-10-080-455-1\_COPY\_52\_177

Perfect score: 675  
Sequence: 1 ERAKEPCMAKFGPLPSKQM.....VLKNTYWGIIILLANQFIS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	11.4	851	2	T51545 receptor protein k
2	75.5	11.2	314	2	I50811 MHC class I protei
3	75.5	11.2	3890	2	C89921 hypothetical prote
4	75	11.1	575	2	T28230 ORF MSV069 probabl
5	74	11.0	233	2	S11688 tumor necrosis fac
6	74	11.0	543	2	S68467 CD40 receptor-asso
7	74	11.0	567	2	I49272 CD40 receptor-asso
8	74	11.0	568	2	A55960 CD40 receptor-asso
9	73.5	10.9	504	2	T47446 hypothetical prote
10	72	10.7	393	2	D75207 hypothetical prote
11	72	10.7	477	2	S32223 penicillin-binding
12	72	10.7	486	2	E35665 penicillin-binding
13	72	10.7	525	2	E70125 hypothetical prote
14	72	10.7	609	1	A43458 conserved hypotet
15	71.5	10.6	1123	2	A72311 intrinsic factor-B
16	71.5	10.6	3623	2	T08618 tumor necrosis fac
17	71	10.5	232	1	S12606 penicillin-binding
18	71	10.5	473	2	S39404 penicillin-binding
19	71	10.5	486	2	D55965 penicillin-binding
20	71	10.5	486	2	B35965 penicillin-binding
21	71	10.5	486	2	B35965 penicillin-binding
22	71	10.5	486	2	B35965 penicillin-binding
23	71	10.5	679	2	S06000 penicillin-binding
24	71	10.5	680	2	G95194 penicillin-binding
25	71	10.5	685	2	T98061 penicillin-binding
26	70.5	10.4	297	2	T28188 hypothetical prote
27	70.5	10.4	890	2	A30481 bacteriocin BCNS -
28	70.5	10.4	1508	2	T31098 probable dextran su
29	70	10.4	1010	2	T33372 hypothetical prote

30	69.5	10.3	234	1	A25451 tumor necrosis fac
31	69.5	10.3	351	2	S67649 MSS2 protein - yea
32	69.5	10.3	989	2	A54505 serine-repeat anti
33	69.5	10.3	997	2	B71617 SERA antigen/papal
34	69.5	10.3	1236	2	B35329 hypothetical prote
35	68.5	10.1	129	2	B35216 FPI4 protein - fow
36	68.5	10.1	187	2	B72666 hypothetical prote
37	68.5	10.1	290	2	S59322 glycoprotein VP7 p
38	68.5	10.1	326	1	VGXK25 glycoprotein VP7 p
39	68.5	10.1	326	1	VGXK35 hypothetical prote
40	68.5	10.1	686	2	T20898 hypothetical prote
41	68.5	10.1	704	2	T29996 cell-cycle-depende
42	68.5	10.1	1017	2	PC4035 tumor necrosis fac
43	68	10.1	1017	2	PC4035 conserved hypotet
44	68	10.1	345	2	B64565 conserved hypotet
45	68	10.1	345	2	E71858 hypothetical prote

## ALIGNMENTS

## RESULT 1

T51545 receptor protein kinase-like protein - Arabidopsis thaliana

N/Alternate names: protein F2K13\_50

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 18-Aug-2000 #sequence\_rev18-Aug-2000 #text\_change 16-Aug-2004

C/Accession: T51545

R/Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew

Submitted to the Protein Sequence Database, August 2000

A/Accession: T51545

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1851 <SNT>

A/Cross-references: UNIPROT:Q9LFL1; EMBL:AJ391141

A/Experimental source: cultivar Columbia; BAC clone F2K13

C/Genetics:

A/Map position: 5

A/Intons: 23/1; 202/2; 371/1; 428/2; 452/2; 476/2; 531/1; 602/3; 645/1; 667/1; 730/2

A/Note: F2K13\_50

C/Superfamily: protein kinase homology

Query Match 11.4%; Score 77; DB 2; Length 851;

Best Local Similarity 28.0%; Pred. No. 19;

Matches 28; Conservative 17; Mismatches 27; Indels 28; Gaps 5;

QY 34 WKLEIQLNGLYL-----YQVAPNANYNDVAPPEVLYKKKMIQTITTKSKIQNGGT 88

Db 88 YTLDELQNRMYMKAVFVYGVY--DGYNDYPSFDLYLGPVKWVRVDEGK-----VNGS 139

QY 89 YE--LHV-----GDTIDLFSHQVLYKNTY 113

Db 140 VEETIHPPSSNSIQICLVKIGNSLPFISALERLRIRNDTY 179

## RESULT 2

MHC class I protein, alpha 1, alpha 2, alpha 3 and transmembrane domains - coelacanth (

C/Species: Latimeria chalumnae (coelacanth)

C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

C/Accession: I50811

R/Betz, U.A.K.; Mayer, W.E.; Klein, J.

Proc. Natl. Acad. Sci. U.S.A. 91, 11065-11069, 1994

A/Title: Major histocompatibility complex class I genes of the coelacanth Latimeria cha

A/Reference number: I50810; MUID:95062206; PMID:7972010

A/Accession: I50811

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-314 <BET>

A/Cross-references: UNIPROT:Q31417; EMBL:U08034; NID:G549857; PIDN:AAA52346.1; PID:G560

A/Genetics:

A/Note: Lach-UB-01

A:introns: 91/1; 183/1; 276/1  
C:superfamily: class I hisocompatibility antigen; immunoglobulin homology

Query Match 11.2%; Score 75.5; DB 2; Length 314;  
Best Local Similarity 34.2%; Pred. No. 8;  
Matches 26; Conservative 9; Mismatches 26; Indels 15; Gaps 5;

QY 4 KPCMAKFGPLPSKQMASSEPPCVNKVSDMKLEILLONGI--YLITGOVAPNANVNDVAP 61  
DB 138 KQIRKVCPCVDEAMSYSE-----DMKQCEIE-GLKKYLITGK--ETLERKVP 185  
QY 62 FEVRLYKKNKMIQTIT 77  
DB 186 -EVRYVDRPDLERNL 200

## RESULT 3

hypothetical protein ebhB [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C:Accession: C89921  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C89921  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-3890 <KIR>

A:Cross-references: UNIPROT:Q9JUS3; GB:BA000018; PID:g13701233; PTDN:BA842528.1; GSPDB:C

A:Experimental source: strain N315  
C:Genetics:

A:Gene: ebhB

Query Match 11.2%; Score 75.5; DB 2; Length 3890;  
Best Local Similarity 27.4%; Pred. No. 1.8e+02;  
Matches 31; Conservative 17; Mismatches 40; Indels 25; Gaps 6;

QY 14 LPSKQWASSEPPCVNKVSDMKLEILLONGIYLITGOVAPNANVNDVAPFEVRLYKKNKMI 73  
DB 952 LPSGWTSMITX-----SDNK-----NGSLAITGRVSMNQAFNSDITFKV---SATDNV 996  
QY 74 QLTNFKSKIONVGTVEHVGDTIDLIENSEHOVLKNTYMGITILLANPQFIS 126  
DB 997 NNTINDSOSKHY---SIHVGR---ISEDAHPIVLGNT--EKVVVAVNPFAVS 1039

## RESULT 4

T28230

ORF MSV069 Probable rifampicin resistance (RIF) protein, Heliothis armigera entomopoxvirus

C:Species: Melanoplus sanguinipes entomopoxvirus

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T28230

R:Afonso, C.L.; Twilman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.; J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.  
A:Reference number: Z20484; MUID:99102612; PMID:9847359

A:Accession: T28230  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-575 <AFPO>

A:Cross-references: UNIPROT:Q9YK23; EMBL:AF063866; NID:g4049647; PTDN:AAC97814.1; PID:g4

C:Genetics:

A:Note: MSV069

C:Superfamily: variola virus N2L protein

Query Match 11.1%; Score 75; DB 2; Length 575;  
Best Local Similarity 23.7%; Pred. No. 19;  
Matches 32; Conservative 21; Mismatches 56; Indels 26; Gaps 6;

QY 18 KQWASSEPPCVN-----KVSMDKLEILLON-GLYLIYGV-----APNANYNDVAPFE 63  
DB 32 YQFTSSSVYENGXYLIYKITDSKLEGCNFFGLITLPEIKIGISIRQSFYKLEEFV 91

QY 64 VRLYKKNKMIQTITLNSKXIO-----NVGTYELHAGDITIDLI-FNSEHOV-----LKN 111  
DB 92 IETINDSVNTITIKKSGLELFEFRSGSKISKIIGNNIDLCSPFTGTADDIIFTSRE 151

QY 112 TYWGIILLANPQFIS 126  
DB 152 IYFPLITIPDNOFIN 166

## RESULT 5

S11688

tumor necrosis factor alpha precursor - cat

C:Species: Felis silvestris catus (domestic cat)

C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C:Accession: S11688

R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A. Nucleic Acids Res. 18, 5563, 1990

A:Title: Gene sequence of feline tumor necrosis factor alpha.  
A:Reference number: S11688; MUID:91016860; PMID:2216740

A:Accession: S11688  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-233 <MCG>

A:Cross-references: UNIPROT:P19101; EMBL:X54000; NID:g1084; PTDN:CAA37948.1; PID:g295777

C:Genetics:

A:introns: 62/3; 78/1; 94/1  
C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
F19/20/Binding site: myristate (lys) (covalent) #status predicted  
F/81/Binding site: carbonylate (Ser) (covalent) #status predicted  
F/145-177/Disulfide bonds: #status predicted

Query Match 11.0%; Score 74; DB 2; Length 233;  
Best Local Similarity 24.4%; Pred. No. 7.8;  
Matches 30; Conservative 21; Mismatches 32; Indels 40; Gaps 6;

QY 30 KVSMDKLEILLONGIYLITGOV-----APNANY---NDVAPFEVRLYKKNKMIQTITNKS 80  
DB 118 ELTDNQKLVSPDGLYLIYSQVLFITGQGPCSTHYVLTTHAISRAVSQTKVNLISAI--KS 175  
QY 81 KIQN-----VGTYELHVGDTID-----LIENSEHOVLKNTYMGIT 116  
DB 176 PCORTEPGARAKWBEPIYIGVFOLEKGRDLSTEINIMPAVLDPAFSGOV-----YFGI 230  
QY 117 ILL 119  
DB 231 IAL 233

## RESULT 6

S68467

CD40 receptor-associated protein CAP-1 - human

C:Species: Homo sapiens (man)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C:Accession: S68467; I53498

R:Sato, T.; Irie, S.; Reed, J.C. FEBS Lett. 358, 113-118, 1995

A:Title: A novel member of the TRAF family of putative signal transducing proteins binds

A:Reference number: I53498; MUID:9512692; PMID:7530216

A:Accession: S68467  
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA  
A:Residues: 1-543 <SAT>

A:Cross-references: UNIPROT:Q13114; EMBL:L38509; NID:g695357; PTDN:AAA68195.1; PID:g695357

A:Experimental source: tissue-type fetal brain  
C:Genetics:

A:Gene: CAP-1  
C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology  
C:Keywords: homodimer; signal transduction; zinc finger



A; Experimental source: strains 5296 and 5302

Experimental sources: UNIPROT:Q01588; EMBL:X67240; NID:g65065; PIDN:CAA47665.1; PID:g65066



A:Note: sequence extracted from NCBI backbone (NCBIN:113390, NCBI:113391)  
A:Note: parts of the sequence determined by protein sequencing  
C:Complex: Replication protein A is a trimer of 70k (A1), 32k (A2), and 14k (A3) chains  
C:Function:  
A:Description: thought to be the eukaryotic equivalent of prokaryotic single-stranded DNA synthesis  
A:Pathway: DNA replication initiation  
C:Superfamily: replication protein A1  
C:Keywords: DNA replication initiation, single-stranded DNA binding, trimer, zinc finger  
F:472-494/Region: zinc finger CCCC motif

Query Match	10.7%;	Score 72;	DB 1;	Length 609;
Best Local Similarity	24.3%;	Pred. No. 40;		
Matches	36;	Conservative	25;	Mismatches 51; Indels 36; Gaps 9;

```

QY 3 AKPPCKAKFGPLPSECKOMASSEPPCKNKSJDKLEIILONGILXYLYGQA-----PNANYND 58
Db 127 APPDASHP-APADSKIQNNNSAPPSPKNR-----GTSKFLGGGSLINTPGGSGSK 174
QY 59 VAPF-EVRLPYKNKDMIQIOT-LTNKSKIQ--NYGVTYELHVGDTID-----LIENSEHQ 106
Db 175 VVFIASLNPYQSQWYVRAVITNKGQIRTWNSREGGKSLIEWDESGEIRATAFNEQAD 234
QY 107 -----VLKNITYW-----GITILANPOFIS 126
Db 235 KFSIIEVKNKVIYFSGKGIITLKNKQYTS 262

```

## RESULT 15

conserved hypothetical protein - *Thermotoga maritima* (strain MSB8)  
 C:Species: *Thermotoga maritima*  
 C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C:Accession: A72311  
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
 C.M.  
 Nature 399, 323-329, 1999  
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
 A:Reference number: A72200; MUID:99287316; PMID:10360571  
 A:Accession: A72311  
 A>Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1123 <ARN>  
 A:Cross-references: UNIPROT:Q9X083; GB:AE001760; GB:AE000512; NID:g4981510; PIDN:AA03606  
 A:Experimental source: strain MSB8  
 C:Genetics:  
 A:Gene: TM0988  
 C:Superfamily: Pyrococcus abyssi hypothetical protein PAB0589

Query Match	10.6%;	Score 71.5;	DB 2;	length 1123;
Best Local Similarity	25.7%;	Pred. No. 94;		
Matches 27;	Conservative 21;	Mismatches 36;	Indels 21;	Gaps 5;

```
QY      18  WQAMASSEPCVNKKSDMKL-EILONCLYLIGQVAPNANIVDVAPEVRLLYNKDKMIOQL 76
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      517 WRVAN-----VTKWVDKSIEELIQSN---YGEI-----WQVLRYVDQLVREKKSITATT 562
```

QY 77 TNKSKIQNVGSGTYELHVGDTIDLIENSEHQVLKNTYWGIIILAN 121  
| | | | : | : | : | :  
Db 563 RGG-----GSTVEEHVRFEEQIVASKEPQELMDNEMVKLFVLVS 601

Search completed: November 2, 2004, 12:59:28  
Job time : 39 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: November 2, 2004, 12:42:32 ; Search time 192 Seconds  
(without alignments)  
377.590 Million cell updates/sec

Title: US-10-080-455-1\_COPY\_52\_177

Perfect score: 675  
Sequence: 1 ETRXPCMAKFGPLPSKQM.....VAKNTYMGIIILANPQFIS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : uniprot\_spprot:\*  
1: uniprot\_spprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	177	1	TN18 HUMAN
2	675	100.0	177	2	AAH63111
3	675	100.0	177	2	AAH63119
4	348	51.6	173	2	Q80Y62
5	348	51.6	173	2	CAE12166
6	348	51.6	173	2	CAE12167
7	344	51.0	173	2	O7TNW2
8	342	50.7	173	2	Q7TS55
9	342	50.7	173	2	AAQ55265
10	108.5	16.1	272	1	TNF5_CHICK
11	86.5	12.8	516	2	Q86IB8
12	85.5	12.7	270	2	Q89BD6
13	83	12.3	599	2	O8IAW5
14	83	12.3	3063	2	Q8QXN1
15	79.5	11.8	459	2	Q8HMY4
16	79.5	11.7	372	1	PROB_OCEITH
17	78.5	11.6	599	2	Q8E0H3
18	78.5	11.6	599	2	Q8E648
19	78	11.6	695	2	O7RI21
20	78	11.6	10746	2	Q6GGX3
21	77	11.4	228	2	Q6FH99
22	77	11.4	368	2	Q6UAA8
23	77	11.4	368	2	AA128927
24	77	11.4	479	2	Q7RB42
25	77	11.4	646	2	Q6MCG4
26	77	11.4	646	2	CA23735
27	77	11.4	813	2	Q6IM89
28	77	11.4	851	2	Q91FLL
29	77	11.4	3064	2	Q8B388
30	76.5	11.3	418	2	Q8RFW2
31	76.5	11.3	739	2	Q6L2Q6

32	76	11.3	390	2	Q615S8	Q61588 streptococc
33	76	11.3	3063	2	Q8QXN2	Q8QXN2 sugarcane m
34	75.5	11.2	270	2	Q72T60	Q72T60 leptospira
35	75.5	11.2	270	2	Q8E293	Q8E293 leptospira
36	75.5	11.2	270	2	AA569768	AA569768 leptospir
37	75.5	11.2	314	2	Q31417	Q31417 latimeria c
38	75.5	11.2	3890	2	Q99U53	Q99U53 staphylococ
39	75.5	11.2	3890	2	Q9A5M1	Q9A5M1 staphylococ
40	75	11.1	233	1	TNFA_FELCA	P19101 felis silve
41	75	11.1	259	2	Q6UD54	Q6UD54 uncultured
42	75	11.1	259	2	AA05186	AA05186 unculture
43	75	11.1	332	2	Q74W75	Q74W75 nanoarchaeu
44	75	11.1	332	2	AA39283	AA39283 nanoarcha
45	75	11.1	422	2	Q7WZ88	Q7WZ88 shewanella

## ALIGNMENTS

## RESULT 1

TN18 HUMAN STANDARD; PRT; 177 AA.

AC Q9UNG2; Q95852;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 18 (Glucocorticoid-induced TNF-related ligand) (hgtrr) (Activation-inducible TNF-related ligand) (AIRRL) (UNQ149/PRO175)  
DE Name=TNFSF18; Synonyms=AITRL, GITRL, TL6;  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
CX [1]  
RN RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Umbilical vein;  
RX MEDLINE=99175482; PubMed=10074428;  
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M., Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;  
RT "Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR.";  
RL Curr. Biol. 9:215-218(1999).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P., Batton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Sehnagiri R., Stammers C., Wiedand D., Woods K., Xie M.-H., Yansura D., Yl S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
[3]  
RP SEQUENCE OF 9-177 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=99156876; PubMed=10037686;  
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Tang I.-K., Kim Y.-J., Xing L., Liu D., Wang S.-X., Kwon B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand.";  
RL J. Biol. Chem. 274:6056-6061(1999).  
CC -!- FUNCTION: Cytokine that binds to TNFRSF18/AITR/GITR. Important for interactions between activated T lymphocytes and endothelial cells and may modulate T lymphocyte survival in peripheral tissues.  
CC -!- SUBUNIT: Homotrimer (Potential).  
CC

```

CC - SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC - TISSUE SPECIFICITY: Expressed at high levels in the small
CC intestine, ovary, testis, kidney and endothelial cells.
CC - INDUCTION: Up-regulated after stimulation by lipopolysaccharides.
CC - SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF125303; AAD22634.1; -
DR EMBL; AY558668; AAO89227.1; -
DR EMBL; AF117713; AAD19695.1; -
DR Genew; HGNC:11932; TNFSF18.
DR MIM; 603898; -
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF-like.
DR InterPro; IPR008983; TNF-like.
DR PROSITE; PS00251; TNF_1; FALSE NEG.
DR PROSITE; PS0049; TNF_2; FALSE NEG.
DR Cytokine; Glycoprotein; signal-anchor; Transmembrane.
FT DOMAIN 1 28 Cytoplasmic (Potential).
FT TRANSMEM 29 49 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 50 177 Extracellular (Potential).
FT CARBOHYD 129 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 161 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 177 AA; 20307 MW; 3D78CE6B90F4C9E3 CRC64;

Query Match 100.0%; Score 675; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIAKEPCAKGKGLPSKQKMASSPPCVNKRYSDWKLETLONGLYITVQVAPNANYNDVA 60
DB 52 EIAKEPCAKGKGLPSKQKMASSPPCVNKRYSDWKLETLONGLYITVQVAPNANYNDVA 111
QY 61 PFEVRLYKXKMDIQTITNKSXKIQNVGTYELHVGPTIDLIINSEHQVKNNTYWGIIILA 120
DB 112 PFEVRLYKXKMDIQTITNKSXKIQNVGTYELHVGPTIDLIINSEHQVKNNTYWGIIILA 171
QY 121 NPQRTS 126
DB 172 NPQRTS 177

RESULT 2
AAH69111 PRELIMINARY; PRT; 177 AA.
AC AAH69111;
DT 24-MAY-2004 (TREMBlrel. 27, Created)
DT 24-MAY-2004 (TREMBlrel. 27, Last sequence update)
DT 24-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE TNFSF18 protein (Fragment).
GN TNFSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Synthetic constructs;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein U.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Synthetic constructs;
RA Strausberg R.;
RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC069111; AAH69111.1; -
FT NON TER 1 1
SQ SEQUENCE 177 AA; 20307 MW; 3D78CE6B90F4C9E3 CRC64;

Query Match 100.0%; Score 675; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIAKEPCAKGKGLPSKQKMASSPPCVNKRYSDWKLETLONGLYITVQVAPNANYNDVA 60
DB 52 EIAKEPCAKGKGLPSKQKMASSPPCVNKRYSDWKLETLONGLYITVQVAPNANYNDVA 111
QY 61 PFEVRLYKXKMDIQTITNKSXKIQNVGTYELHVGPTIDLIINSEHQVKNNTYWGIIILA 120
DB 112 PFEVRLYKXKMDIQTITNKSXKIQNVGTYELHVGPTIDLIINSEHQVKNNTYWGIIILA 171
QY 121 NPQRTS 126
DB 172 NPQRTS 177

RESULT 3
AAH69319 PRELIMINARY; PRT; 177 AA.
AC AAH69319;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE TNFSF18 protein.
GN TNFSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Phay J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN (2)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RA Strausberg R.;  
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC069319, AAH69319.1, - 3D78CEB9074C9E3 CRC64;  
 SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB9074C9E3 CRC64;

Query Match 100.0%; Score 675; DB 2; Length 177;  
 Best local Similarity 100.0%; Pred. No. 1,1e-57;  
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETAKPEQMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGQVAPNANYNDVA 60  
 DB 52 ETAKPEQMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGQVAPNANYNDVA 111  
 QY 61 PFEVRLYKXKMDIQTITNKSQIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIILA 120  
 DB 112 PFEVRLYKXKMDIQTITNKSQIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIILA 171

QY 121 NPOFIS 126  
 DB 172 NPOFIS 177

RESULT 4  
 ID 080YG2 PRELIMINARY; PRT; 173 AA.  
 AC 080YG2;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE GTR ligand.  
 GN Name=Thsf18; Synonyms=tnsf 18;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CBA/23;  
 RA Bianchini R., Nocentini G., Ronchetti S., Ayroldi E., Riccardi C.;  
 RL Submitted (Feb-2003) to the EMBL/GenBank/DBJ databases.  
 RL (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBA/Ca;  
 RX PubMed=14608036;  
 RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,  
 RA Waldmann H.;  
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is  
 a costimulatory for T cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).

DR EMBL: AY234223; AA089011.1; -  
 DR EMBL: AJ577579; CAE12166.1; -  
 DR EMBL: AJ577580; CAE12167.1; -  
 DR MGI: 2673064; Tnfrsf18.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO: GO:0006955; P:immune response; IEA.  
 DR InterPro: IPR008983; TNF-like.  
 DR InterPro: IPR003636; TNF\_subf.1.  
 DR ProDom: PD002012; TNF\_subf.1.  
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 51.6%; Score 348; DB 2; Length 173;  
 Best local Similarity 56.7%; Pred. No. 7.5e-26;

Matches 72; Conservative 14; Mismatches 39; Indels 2; Gaps 2;  
 QY 2 TAKEPCMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGQVAPNANYNDV 59  
 DB 47 TAKEPCMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGQVAPNANYNDV 106  
 QY 60 APEVRLYKXKMDIQTITNKSQIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIILA 119  
 DB 107 APEVRLYKXKMDIQTITNKSQIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIILA 166  
 QY 120 ANPOFIS 126  
 DB 167 PDLPTIS 173

RESULT 5  
 ID CAE12166 PRELIMINARY; PRT; 173 AA.  
 AC CAE12166;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE GTR ligand.  
 GN TNFSF 18.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CBA/Ca;  
 RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,  
 RA Waldmann H.;  
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is  
 a costimulatory for T cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).  
 DR EMBL: AJ577579; CAE12166.1; -  
 KW Alternative splicing.  
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACF424D2 CRC64;

Query Match 51.6%; Score 348; DB 2; Length 173;  
 Best local Similarity 56.7%; Pred. No. 7.5e-26;  
 Matches 72; Conservative 14; Mismatches 39; Indels 2; Gaps 2;

QY 2 TAKEPCMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGQVAPNANYNDV 59  
 DB 47 TAKEPCMAKFGPLPSKQWQASSEPPCVNKSVDWKLEIIQNGLYLYIGQVAPNANYNDV 106  
 QY 60 APEVRLYKXKMDIQTITNKSQIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIILA 119  
 DB 107 APEVRLYKXKMDIQTITNKSQIQNVGTYELHVGDTIDLIENSEHOVLKNNYWGIIILA 166  
 QY 120 ANPOFIS 126  
 DB 167 PDLPTIS 173

RESULT 6  
 ID CAE12167 PRELIMINARY; PRT; 173 AA.  
 AC CAE12167;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE GTR ligand.  
 GN TNFSF 18.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CBA/Ca;

RA Tone M., Tone Y., Adams E., Yates S.F., Frewin M.R., Cobbold S.P.,  
 RA Waldmann H.,  
 RT "Mouse glucocorticoid-induced tumor necrosis factor receptor ligand is  
 RT costimulatory for T cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15059-15064(2003).  
 DR EMBL: A0577580; CAB12167.1; -.  
 KW Alternative splicing.  
 SQ SEQUENCE 173 AA; 19745 MW; 1FD2294CACC424D2 CRC64;

Query Match 51.6%; Score 348; DB 2; Length 173;  
 Best Local Similarity 56.9%; Pred. No. 7.5e-26;  
 Matches 72; Conservative 14; Mismatches 39; Indels 2; Gaps 2;

QY 2 TAKEPCMAKFGPLPSKQWMASSPPCVNKVSDMKLEITIQNGLYLYGVAP-NANY-NDV 59  
 DB 47 TAISCSWKFELSSSKMHMTSPKHCVTTSDDGKLKILQSGTYLYIGGVIPVDKRYIKDN 106  
 QY 60 APEFVRLYKKNKMTQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIIL 119  
 DB 107 APEFVQIYKKNDVLTQTLNDFQILPIGVYELHAGDNILKFNKSDHIQKNNYWGIIIL 166  
 QY 120 ANPOFIS 126  
 DB 167 PDLFFIS 173

RESULT 7  
 Q7TNY2 PRELIMINARY; PRT; 173 AA.  
 AC Q7TNY2;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE GTR ligand.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX PubMed=14647196;  
 RA Kim J.D., Choi B.K., Bae J.S., Lee U.H., Han I.S., Lee H.W.,  
 RA Youn B.S., Vinay D.S., Kwon B.S.;  
 RT "Cloning and characterization of GTR ligand."  
 RL Genes Immun. 4:564-569(2003).  
 DR EMBL: AY267900; AAP6745.1;  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO: GO:0006955; P:immune response; IEA.  
 DR InterPro: IPR003636; TNF subf.  
 DR Prodom: PD002012; TNF subf. 1.  
 SQ SEQUENCE 173 AA; 19773 MW; 1FD22953BCFC34C5 CRC64;

Query Match 51.0%; Score 344; DB 2; Length 173;  
 Best Local Similarity 55.9%; Pred. No. 1.8e-25;  
 Matches 71; Conservative 14; Mismatches 40; Indels 2; Gaps 2;

QY 2 TAKEPCMAKFGPLPSKQWMASSPPCVNKVSDMKLEITIQNGLYLYGVAP-NANY-NDV 59  
 DB 47 TAISCSWKFELSSSKMHMTSPKHCVTTSDDGKLKILQSGTYLYIGGVIPVDKRYIKDN 106  
 QY 60 APEFVRLYKKNKMTQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIIL 119  
 DB 107 APEFVQIYKKNDVLTQTLNDFQILPIGVYELHAGDNILKFNKSDHIQKNNYWGIIIL 166  
 QY 120 ANPOFIS 126  
 DB 167 PDLFFIS 173

RESULT 8  
 Q7TNS5

ID Q7TNS5 PRELIMINARY; PRT; 173 AA.

AC Q7TNS5;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE GTR ligand (Glucocorticoid-induced-tumor necrosis factor receptor  
 DE ligand).  
 GN Name=Gtr1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57/BL6; TISSUE=Spleen;  
 RA J.H., Terhorst C.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/O;  
 RX MEDLINE=22883945; PubMed=14521928;  
 RA Yu K.-Y., Kim H.S., Song S.-Y., Min S.S., Jeong J.J., Youn B.S.;  
 RT "Identification of a ligand for glucocorticoid-induced tumor necrosis  
 RT factor receptor constitutively expressed in dendritic cells."  
 RL Biochem. Biophys. Res. Commun. 310:433-438(2003).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/O;  
 RA Yu K.-Y., Min S.S., Youn B.-S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY320040; AAP70494.1; -.  
 DR EMBL: AY359852; AAQ55265.1; -.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO: GO:0006955; P:immune response; IEA.  
 DR InterPro: IPR003636; TNF subf.  
 DR Prodom: PD002012; TNF subf. 1.  
 KW Receptor.  
 SQ SEQUENCE 173 AA; 19732 MW; 0F08494CACC424D2 CRC64;

Query Match 50.7%; Score 342; DB 2; Length 173;  
 Best Local Similarity 55.9%; Pred. No. 2.9e-25;  
 Matches 71; Conservative 14; Mismatches 40; Indels 2; Gaps 2;

QY 2 TAKEPCMAKFGPLPSKQWMASSPPCVNKVSDMKLEITIQNGLYLYGVAP-NANY-NDV 59  
 DB 47 TAISCSWKFELSSSKMHMTSPKHCVTTSDDGKLKILQSGTYLYIGGVIPVDKRYIKDN 106  
 QY 60 APEFVRLYKKNKMTQTLTNKSKIQNVGTYELHVGDTIDLFNSEHQVLKNNYWGIIIL 119  
 DB 107 APEFVQIYKKNDVLTQTLNDFQILPIGVYELHAGDNILKFNKSDHIQKNNYWGIIIL 166  
 QY 120 ANPOFIS 126  
 DB 167 PDLFFIS 173

RESULT 9  
 AAQ55265 PRELIMINARY; PRT; 173 AA.  
 ID AAQ55265;  
 AC AAQ55265;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE Glucocorticoid-induced-tumor necrosis factor receptor ligand.  
 GN GTR1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=129/J;  
 RX MEDLINE=22883945; PubMed=14521928;  
 RA Yu K.-Y., Kim H.S., Song S.-Y., Min S.S., Jeong J.-J., Youn B.S.;  
 RT "Identification of a ligand for glucocorticoid-induced tumor necrosis  
 factor receptor constitutively expressed in dendritic cells";  
 RL Biochem. Biophys. Res. Commun. 310:433-438(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/J;  
 RA Yu K.-Y., Min S.S., Youn B.-S.;  
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; A3359852; AAC55265.1; -  
 KW Receptor.  
 SQ SEQUENCE 173 AA; 19732 MW; 0F08494CACAC424D2 CRC64;  
 Query Match 50.7%; Score 342; DB 2; Length 173;  
 Best Local Similarity 55.9%; Pred. No. 2.9e-25;  
 Matches 71; Conservative 14; Mismatches 40; Indels 2; Gaps 2;  
 QY 2 TAKEPCMAKFGPIPSKQMASSSEPPCVNKKVSDMKLEILLQNGLYLYGQVAP-NANV-NDV 59  
 DB 47 TATESCMVKEFLSSSSKHMSTPKPHCVNTSDGKILQSGYLYGQVLPVKKYIKDN 106  
 QY 60 APPPEVLYKKKMDIQTITNSKIQNVGTYELHVGDTIDLFNSEHQVLKNTYMGIIIL 119  
 DB 107 APPVQVYKKNDVLTQIMNDPQILPIGVTYELHAGDNITYKKNSKHIOKNTYMGIIIM 166  
 QY 120 ANPQFIS 126  
 DB 167 PDLPIFS 173  
 RESULT 10  
 TNFS CHICK STANDARD; PRT; 272 AA.  
 ID TNFS CHICK  
 AC Q91B8; 2003 (Rel. 41, Created)  
 DT 28-FEB-2004 (Rel. 43, Last sequence update)  
 DE 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-  
 DE L) (CD154 protein).  
 GN Name=TNFSF5; Synonyms=CD40LG, CD40L;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=White Leghorn; TISSUE=Spleen;  
 RA Tregaskes C.A., Young J.R., Burnside J.;  
 RT "Cloning of a putative chicken CD40 ligand."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell  
 proliferation in the absence of IL-4. Involved in immunoglobulin  
 production in the presence of IL-4.  
 CC class switching (By similarity).  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 extracellular soluble form (By similarity).  
 CC -1- PTM: The soluble form derives from the membrane form by  
 proteolytic processing (By similarity).  
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; AJ243435; CAB95748.2; -

DR HSSP; P29965; 119R.  
 DR GO; GO:0016021; C:integral to membrane; ISS.  
 DR GO; GO:0005174; F:CD40 receptor binding; ISS.  
 DR GO; GO:0042100; P:B-cell proliferation; ISS.  
 DR GO; GO:0006954; P:inflammatory response; ISS.  
 DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.  
 DR GO; GO:0030168; P:platelet activation; ISS.  
 DR InterPro; IPR003263; TNF\_5.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_1like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01702; CD40LIGAND.  
 DR Prodom; PD008600; TNF\_5; 1.  
 DR Prodom; PD002012; TNF\_subf; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS00469; TNF\_2; 1.  
 KW Cytokine; Glycoprotein; Signal-anchor; Transmembrane.  
 FT CHAIN 1 272  
 FT CHAIN 111 272  
 FT DOMAIN 1 23  
 FT TRANSMEM 24 44  
 FT DOMAIN 45 272  
 FT SITE 110 111  
 FT DISULFID 190 229  
 FT CARBOHYD 124 124  
 FT CARBOHYD 146 146  
 FT CARBOHYD 251 251  
 SQ SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;  
 Query Match 16.1%; Score 108.5; DB 1; Length 272;  
 Best Local Similarity 29.8%; Pred. No. 0.027;  
 Matches 36; Conservative 22; Mismatches 44; Indels 19; Gaps 5;  
 QY 17 KQWASSEPPCVNKKVSDMKLEILLQNGLYLYGQVAPNANVNDVAFERLY----- 67  
 DB 153 KMTSYAPTSLSISYHEGKLVKAGLYIYSQVFCRKAASAFETLYIYLPME 211  
 QY 68 -----KKKMDIQTITNSKIQNV--GGTYELHVGDT--IDLFNSEHQVLKNTYMGIIIL 118  
 DB 212 DRLMKGLDTHSTALCELQSIREGVPELRQGMVFVNTDSTAVNVPNGNTYFGCFK 271  
 QY 119 L 119  
 DB 272 L 272  
 RESULT 11  
 ID Q961B8 PRELIMINARY; PRT; 516 AA.  
 AC Q961B8;  
 DT 01-JUN-2003 (TRENDEL. 24, Created)  
 DT 01-JUN-2003 (TRENDEL. 24, Last sequence update)  
 DT 01-MAR-2004 (TRENDEL. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX4;  
 RX MEDLINE=22092622; PubMed=12097910;  
 RA Gloeckner G., Eichinger L., Szafarski K., Pachebat J., Dear P.,  
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,  
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;  
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum";  
 RL Nature 418:79-85(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX4;

RA Baumgart C.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC116551; AAO52204.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 516 AA; 58667 MW; 80B308CF6CDF97C2 CRC64;  
Query Match 12.8%; Score 86.5; DB 2; Length 516;  
Best Local Similarity 29.0%; Pred. No. 7.9;  
Matches 27; Conservative 17; Mismatches 36; Indels 13; Gaps 3;  
QY 29 NKVSDMKLEILQNGVYLYIGQVAPNPNYVAPFEVRLYKNNKMIQTLLNKSQIQNVGT 88  
DB 419 NKTBDKSLTF-----LYTY-----NIEKQVQPOVTYIEFCTDEINEMITKFOIENNDD 469  
QY 89 YELHVGDTIDLIENSEHOVLKNNYTWGIILLAN 121  
DB 470 VNNINEXKNDIFLN-----IPKQDNCQGIILLTN 498  
RESULT 12  
ID Q896D6 PRELIMINARY; PRT; 270 AA.  
AC Q896D6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DE K1LA protein, putative phage-related DNA binding protein.  
GN Name=k1LA; Ordered locus names=CTC01071;  
OS Clostridium tetani.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_Taxid=1513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Massachusetts / B88;  
RX MEDLINE=22457253; PubMed=12552129;  
RA Bruggemann H., Baerner S., Fricke W.F., Wierzer A., Liesegang H.,  
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,  
RA Gottschalk G.;  
RT "The genome sequence of Clostridium tetani, the causative agent of  
RT tetanus disease.";  
RT Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).  
DR EMBL; AEO15939; AAO35658.1; -  
DR InterPro; IPR003497; BRO-N; 1.  
DR Pfam; PF02498; Bro-N; 1.  
KW Complete proteome.  
SQ SEQUENCE 270 AA; 31533 MW; C378AB524C0133A8 CRC64;  
Query Match 12.7%; Score 85.5; DB 2; Length 270;  
Best Local Similarity 25.4%; Pred. No. 4.7;  
Matches 31; Conservative 18; Mismatches 36; Indels 37; Gaps 5;  
QY 30 KVSQDKLEILQNGVYLYIGQVAPNPNYVAPFEVRLYKNNKMIQTLLNKSQIQNVGT 88  
DB 134 KAKKMKLEILQNGVYLYIGQVAPNPNYVAPFEVRLYKNNKMIQTLLNKSQIQNVGT 186  
QY 89 -----YELHVG-----DTIDLIENSEHOVLKNNYTW-----GIILL 119  
DB 187 LNKLLHKLKVOYKQNDQWLTKYKRSKGYTSETIDIVRSQGRPDVKNNTKQTKGRFL 246  
QY 120 AN 121  
DB 247 YN 248  
RESULT 13  
ID Q81AW5 PRELIMINARY; PRT; 599 AA.  
AC Q81AW5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein PF08\_0083.

GN Name=PF08\_0083;  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_Taxid=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,  
RA Quail M., Bartell B.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL844507; CAD51245.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 599 AA; 70706 MW; B50A265C5D01AE28 CRC64;  
Query Match 12.3%; Score 83; DB 2; Length 599;  
Best Local Similarity 22.9%; Pred. No. 21;  
Matches 32; Conservative 24; Mismatches 32; Indels 52; Gaps 6;  
QY 28 VNKSPDKLEILQNGVYLYIGQVAPNPNY--NDVAFPEVRLYKNNKMIQTLLNKSQIQNVGT 76  
DB 409 KNNMSN--MSNNNNRLLYLNNKSSLNNNYSNNIKPLYNQYQYNNKLLYNTLNHNNQNPNG 466  
QY 77 -----TNKSKI-----QNVGTYELHVGDTIDLIENSEHOVLK-- 109  
DB 467 KMSFDNNIPSSNNKKNYKNNKSTYLLNNLNKNSGSGLLHSGNNMLCYSOQNSLNDM 526  
QY 110 -----NNTYWGIIILLANPOF 124  
DB 527 NREHDNNMY-----NPDF 539  
RESULT 14  
ID Q8QXN1 PRELIMINARY; PRT; 3063 AA.  
AC Q8QXN1;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Polyprotein.  
OS Sugarcane mosaic virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;  
OC Polyvirus.  
OX NCBI\_Taxid=12224;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22105130; PubMed=12111432;  
RA Chen U., Chen U.P., Adams M.U.;  
RT "Characterisation of polyviruses from sugarcane and maize in China.";  
RL Arch. Virol. 147:1237-1246(2002).  
CC -!- SIMILARITY: Belongs to the polyviruses polyprotein family.  
DR EMBL; AJ310105; CAC84095.1; -  
DR HSSP; P04517; IJVM.  
DR MEROPS; C06.001; -.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.  
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR GO; GO:0019079; P:viral genome replication; IEA.  
DR InterPro; IPR001410; DEAD.  
DR InterPro; IPR011545; DEAD/DEAH N.  
DR InterPro; IPR001650; Helicase C.  
DR InterPro; IPR001730; Peptidase C4.  
DR InterPro; IPR001456; Peptidase C6.  
DR InterPro; IPR002540; pept\_S30\_Polc\_P1.  
DR InterPro; IPR001592; Poly\_coat.  
DR InterPro; IPR007095; RNA\_pol\_DS\_PS.  
DR InterPro; IPR001205; RNA\_pol\_P3D.  
DR InterPro; IPR007094; RNA\_pol\_Psv1r.



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DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF00851; Peptidase_C6; 1.
DR Pfam; PF00767; Polypeptidase; 1.
DR Pfam; PF01577; Poly P1; 1.
DR Pfam; PF00680; RNA-dep. RNA pol; 1.
DR PRINTS; PR00966; NIAOTYPTASE.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR ATP-binding; Coat protein; Helicase; Hydrolase; Polypeptidase.
FT CHAIN 694 1040
FT CHAIN 1041 1107
FT CHAIN 1108 1145
FT CHAIN 1146 1198
FT CHAIN 1199 1229
FT CHAIN 1230 1233
FT CHAIN 1234 1250
FT CHAIN 1251 1303
FT CHAIN 1304 1363
SQ SEQUENCE 3063 AA; 346241 MW; E6019C8D1E80B59D CRC64;

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Query Match 12.3%; Score 83; DB 2; Length 3063;
Best local similarity 29.2%; Pred. No. 1.4e+02;
Matches 35; Conservative 15; Mismatches 50; Indels 20; Gaps 5;

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QY 4 KEPGAKGFLPSPKQMASSPPCVNKSVDWKLFIQNGLYLIGQVAPNANVDVAFPE 63
DB 338 KERCNPFSSHPLMQVAVETIGHTDNO SKQILDI-SALAKVMTTPDDVAKASVALL 396
QY 64 V-RLYKXK-----DMIGTLNKSQIONVGATYELAHVGDITDIFNSEHQVLYKN-NTYWG 115
DB 397 VSRWYKXKESLKTDTLETFRNKVSPKS-----TINAAIMCNDQIDKNAIFVWG 445

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## RESULT 15

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ID Q6HHM4 PRELIMINARY; PRT; 459 AA.
AC Q6HHM4;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Dihydrolysoamide dehydrogenase (EC 1.8.1.4).
GN Name=accl; ORFNames=BT9727.2536;
OS Bacillus thuringiensis serovar konkukian str. 97-27.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus thuringiensis serovar konkukian.
OX NCBI_TaxID=281309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka K.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Protein N(6)-(dihydrolysoyl) lysine + NAD(+) =
CC protein N(6)-(lipoyl) lysine + NADH.
CC -1- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -1- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -1- MISCELLANEOUS: The active site is a redox-active disulfide bond
CC (By similarity).
CC -1- SIMILARITY: Belongs to the class-I pyridine nucleotide-disulfide
CC oxidoreductase family.
DR EMBL; AE017355; AAT61350.1; -.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR000815; Hg_reductase.
DR InterPro; IPR006258; Lipoamide_dh.
DR InterPro; IPR000205; NAD_BS.
DR InterPro; IPR000103; Pyridine_redox_2.
DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR004099; Pyr_redox_dim.
DR Pfam; PF00070; Pyr_redox; 1.

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DR Pfam; PF02852; Pyr_redox_dim; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00945; HGRDPTASE.
DR PRINTS; PR00411; PNDRDPTASE.
DR PRINTS; PR00469; PNDRDPTASE.
DR PRINTS; PR000139; FAD_pyr_redox; 1.
DR TIGRFAMs; TIGR01350; Lipoamide DH; 1.
DR PROSITE; PS00076; PYRIDINE_REDOX_1; UNKNOWN 1.
DR FAD; Flavoprotein; NAD; Oxidoreductase; Redox-active center.
SQ SEQUENCE 459 AA; 49338 MW; B9F86C0FC93DD331 CRC64;

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```

Query Match 11.8%; Score 79.5; DB 2; Length 459;
Best local similarity 25.4%; Pred. No. 33;
Matches 32; Conservative 25; Mismatches 56; Indels 13; Gaps 6;

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QY 5 EPGAKGFLPSPKQMASSPPCVNKSVDWKLFIQNGLYLIGQVAPNANVDVAFPE 59
DB 144 EPARLPAPDPGKWLINSSHAMSLNIPK-SLLIVGGGVIGCFEASISYSLGTQVIVEM 202
QY 60 APFEVRLYKNKMDIQTITNKSQIONVGATYELAHVGDITDIFNSEHQVLYKNNTYWG 119
DB 203 AP-QLLPGEEDIDIAIIL--KEKESDG--VEIFGAALKGLNRYKKA--SFYKGSIQE 255
QY 120 ANPQFI 125
DB 256 ANPEYV 261

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Search completed: November 2, 2004, 12:58:45
Job time : 194 secs

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